

GenCore version 5.1.6
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3M nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:56:32 : Search time 49.5831 Seconds
(without alignments)
5849.036 Million cell updates/sec

File: US-09-816-391A-1_COPY_472_600

Perfect score: 129
Sequence: 1 tgaacttcgtcgttagcga.....tattccgagctagtcagc 129

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	129	100.0	600	US-09-816-391A-1	Sequence 1, Appl
2	28.4	22.0	936	US-09-903-410-31	Sequence 31, Appl
3	28.4	22.0	936	US-10-027-805-31	Sequence 31, Appl
4	28.4	22.0	936	US-10-027-804-31	Sequence 31, Appl
5	28.4	22.0	2451	US-09-938-842A-64	Sequence 64, Appl
6	27.8	20.37	12	US-10-199-672-591	Sequence 591, App
7	27.8	20.37	12	US-10-187-749-591	Sequence 591, App
8	27.8	20.37	13	US-10-194-457-591	Sequence 591, App
9	27.8	20.37	12	US-10-052-586-591	Sequence 591, App
10	27.8	20.37	14	US-10-174-590-591	Sequence 591, App
11	27.8	20.37	14	US-10-176-758-591	Sequence 591, App
12	27.8	20.37	14	US-10-175-737-591	Sequence 591, App
13	27.8	20.37	14	US-10-173-706-591	Sequence 591, App
14	27.8	20.37	14	US-10-175-736-591	Sequence 591, App
15	27.8	20.37	14	US-10-175-752-591	Sequence 591, App
16	27.8	20.37	14	US-10-176-482-591	Sequence 591, App

C 17	27.8	21.6	2037	14	US-10-176-757-591	Sequence 591, App
C 18	27.8	21.6	2037	14	US-10-176-913-591	Sequence 591, App
C 19	27.8	21.6	2037	14	US-10-180-552-591	Sequence 591, App
C 20	27.8	21.6	2037	14	US-10-180-557-591	Sequence 591, App
C 21	27.8	21.6	2037	14	US-10-173-700-591	Sequence 591, App
C 22	27.8	21.6	2037	14	US-10-174-572-591	Sequence 591, App
C 23	27.8	21.6	2037	14	US-10-174-576-591	Sequence 591, App
C 24	27.8	21.6	2037	14	US-10-174-582-591	Sequence 591, App
C 25	27.8	21.6	2037	14	US-10-174-588-591	Sequence 591, App
C 26	27.8	21.6	2037	14	US-10-175-739-591	Sequence 591, App
C 27	27.8	21.6	2037	14	US-10-175-740-591	Sequence 591, App
C 28	27.8	21.6	2037	14	US-10-175-743-591	Sequence 591, App
C 29	27.8	21.6	2037	14	US-10-176-488-591	Sequence 591, App
C 30	27.8	21.6	2037	14	US-10-176-492-591	Sequence 591, App
C 31	27.8	21.6	2037	14	US-10-176-747-591	Sequence 591, App
C 32	27.8	21.6	2037	14	US-10-176-750-591	Sequence 591, App
C 33	27.8	21.6	2037	14	US-10-176-985-591	Sequence 591, App
C 34	27.8	21.6	2037	14	US-10-176-987-591	Sequence 591, App
C 35	27.8	21.6	2037	14	US-10-176-992-591	Sequence 591, App
C 36	27.8	21.6	2037	14	US-10-176-993-591	Sequence 591, App
C 37	27.8	21.6	2037	14	US-10-184-658-591	Sequence 591, App
C 38	27.8	21.6	2037	14	US-10-173-695-591	Sequence 591, App
C 39	27.8	21.6	2037	14	US-10-173-695-591	Sequence 591, App
C 40	27.8	21.6	2037	14	US-10-173-697-591	Sequence 591, App
C 41	27.8	21.6	2037	14	US-10-173-705-591	Sequence 591, App
C 42	27.8	21.6	2037	14	US-10-174-576-591	Sequence 591, App
C 43	27.8	21.6	2037	14	US-10-174-585-591	Sequence 591, App
C 44	27.8	21.6	2037	14	US-10-174-586-591	Sequence 591, App
C 45	27.8	21.6	2037	14	US-10-175-747-591	Sequence 591, App

ALIGNMENTS

RESULT 1
US-09-816-391A-1
Sequence 1, Application US/09816391A
Patient No. US20020054865A1
GENERAL INFORMATION:
APPLICANT: FUJIMORI, Minoru
APPLICANT: TANIGUCHI, Shunichiro
APPLICANT: ANANO, Jun
APPLICANT: YAZAWA, Kazuyuki
APPLICANT: KANO, Yasunobu
APPLICANT: NAKAMURA, Toshiyuki
APPLICANT: SASAKI, Takayuki
TITLE OF INVENTION: Anaerobic bacterium as a drug for cancer gene therapy
FILE REFERENCE: 2001-FMC/01736
CURRENT APPLICATION NUMBER: US/09/816,391A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 00/287688
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 1
LENGTH: 600
TYPE: DNA
ORGANISM: Bifidobacterium longum
FEATURE:
NAME/KEY: CDS
LOCATION: (193)..(471)
US-09-816-391A-1

Query Match 100.0%; Score 129; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGAACCTTCGCTGATGACATTCGAGCATTCGAGCAAGACCCGACGAGA 60
DB 472 TGACCTTCGCTGATGACATTCGAGCATTCGAGCAAGACCCGACGAGA 531
OY 61 TGGTCGGGGGCTTTTGTGTGTGCTGTGACGTGTGCCAACCGTATTTATCCGACT 120
DB 532 TGGTCGGGGGCTTTTGTGTGTGCTGTGACGTGTGCCAACCGTATTTATCCGAGCT 591

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HATLE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
REGISTRATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 936 NUCLEOTIDES
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: GENOMIC DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
-804-31

Query Match	22.0%;	Score 28.4;	DB 14;	Length 936;
Best Local Similarity	56.4%;	Pred. No. 2.3;		
Matches 53;	Conservative 0;	Mismatches 41;	Indels 0;	Gaps 0;

2 GACCTTTCGCGCTAGGCGATTACTTCGAGCACTTCTACACGAAGAAGCCCCGACCCGAGAT 61
 11
 718 GACCTTGGAGACCTACCTCCTCGCCTGATCATTAACCGCCGCAATACGACCCCGCTGAGAGAT 777
 62 GCTCGGGCTCTTTTGT 95
 11
 778 GAAGGAGAGATTTCGGGCACATGCTGGAAAGAG 811

RESULT 5
JCS-09-938-842A-64
; Sequence 64, Application US/09938842A
; Patent No. US20020160378A1
GENERAL INFORMATION:

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1  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
2  TITLE OF INVENTION: SAME, AND METHODS OF USE
3  FILE REFERENCE: SCRIPT300-5
4  CURRENT APPLICATION NUMBER: US/09/938,842A
5  CURRENT FILING DATE: 2001-08-24
6  PRIOR APPLICATION NUMBER: US 60/227,866
7  PRIOR FILING DATE: 2000-08-24
8  PRIOR APPLICATION NUMBER: US 60/264,647
9  PRIOR FILING DATE: 2001-01-16
10 PRIOR APPLICATION NUMBER: US 60/300,111
11 PRIOR FILING DATE: 2001-06-22
12 NUMBER OF SEQ ID NOS: 5379
13
14 SEQ ID NO 64
15     LENGTH: 2451
16     TYPE: DNA
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18 ORGANISM: Arabidopsis thaliana
19
20 S-O9-938-842A-64

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Query Match	22.0%	Score 28.4;	DB 10;	Length 2451;
Best Local Similarity	53.6%	Pred. No. 3.2;		
Matches	59;	Conservative	0;	Mismatches 51;
			Indels	0;
			Gaps	0;

791 TGGCTCCTCGTGCAAGGATTGCATTTACAAAGCTCTTACCAGACTTTTTGAAGGCCTTG **850**

QY 75 TTGTTGTGGTCTGTAGCTGTTGTCCAACCGTAATATTCCGACTAGTT 124
| | | | | | | | | | | | | | |
Db 851 TAGCTGATGTGGTGGCTGCCATTGATCAGGCTGTCATGATGAGTAGAT 900

RESULT 6
US-10-199-672-591/c

Sequence 591, Application US/10199672
Publication No. US20030148442A1
GENERAL INFORMATION:
Inventor: Robert Zende B

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3430R1C1
 CURRENT APPLICATION NUMBER: US/10/199 673

CURRENT APPLICATION NUMBER: US/10/199,672

CURRENT FILING DATE: 2002-0/-18
PRIOR APPLICATION NUMBER: US/10/052,586

PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 199/-10-1/
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 199/-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-20

PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-26
Remaining Prior Application data re
NUMBER OF SEQ ID NOS: 613

NUMBER OF SEQ ID NOS: 612
SEQ ID NO 591
LENGTH: 2037

LENGTH: 203/
TYPE: DNA
ORGANISM: Homo Sapien

ORGANISM: HOMO SAPIEN
S-10-199-672-591

Query Match	21.6%	Score
Post 10001 4441 21444	57.5%	Prod

Best Local Similarity 57.5%; Frequent
Matches 50; Conservative 0; M

42 ACAAGACCCCGACCGAGATGTC

b 1335 AAAAAGACCATCATCTACATTGTC

102 AACCGTATTATCCGGACTAGTTC

b 1275 CTGTTGCTATCTGGACTAATGCC

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RESULTS /
MS-10-187-749-591/c
Sequence 501 200102440 MS/1018774

GENERAL INFORMATION:
sequence 591, Application US/1018774
Publication No. US20030153036A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 ABBREVIATION: Chon Tian

APPLICANT: Coddard, Andrew
APPLICANT: Desnoyers, Luc
APPLICANT: Chen, Yolan

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin D.

APPLICANT: Sunney, Aubrey D.
APPLICANT: Pan, James
APPLICANT: Smith, Victor L.

AFFILIATION: SMITHSONIAN VACCINATOR

APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/187,749
PRIORITY FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059253
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQUENCE ID NO 591
LENGTH: 2037
TYPE: DNA
ORGANISM: Homo Sapien
S-10-187-749-591

Query Match 21.6%; Score 27.8; DB 12; Length 2037;
Best Local Similarity 57.5%; Pred. No. 5.1;
Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

X 42 ACAAGACCCGACCGATGTGGGGCTTTTGTGTGCTGTGCAGTGTC 101
 | | | | | | | | | | | | | | | | | | | | | |
Y 1335 AAAAAGGCCATCATCTCAATTGTCAGGGCACATATCTGTGGTAGCTGTGCC 1276
 | | | | | | | | | | | | | | | | | | | | | |
Y 102 AACGTAATTATTCGGACTGTGCAGC 128
 | | | | | | | | | | | | | | | | | | | | | |
b 1275 CTGTTGCTACTGTGGAGCTATATGCTATC 1249

ESULT 8
S-10-194-457-591/C
Sequence 591, Application US/10194457
Publication No. US20030153037A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C296
CURRENT APPLICATION NUMBER: US/10/194,457
PRIORITY FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263

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PRIORITY FILLING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 591
LENGTH: 2037
TYPE: DNA
ORGANISM: Homo Sapien
US-10-194-457-591

Query Match      21.6%; Score 27.8; DB 12; Length 2037;
Best Local Similarity 57.5%; Pred. No. 5.1;
Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

OY      42 ACAAGACCCGCGACGATGGTCGGGGCTTTTGTGTGGCGCCTGACGCTGTCC 101
Db       1335 AAAAAGCCATCATCTCACTTGCTCAGGCTACTTAATCTGTCTCAGTGGCTTCCC 1276
OY      102 AACCGTATTATTCGCGACTAGTTCAGC 128
Db       1275 CTGTTGCTATCTGGGACTAATGCATC 1249

RESULT 9
US-10-052-586-591/c
Sequence 591, Application US/10052586
Publication No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
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PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/0835559
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PRIOR APPLICATION NUMBER:	60/084366
PRIOR FILING DATE:	1998-05-05
PRIOR APPLICATION NUMBER:	60/084414
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PRIOR APPLICATION NUMBER:	60/0846539
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PRIOR APPLICATION NUMBER:	60/085573
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085579
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085580
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085700
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/086023
PRIOR FILING DATE:	1998-05-18
PRIOR APPLICATION NUMBER:	60/086392
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/086486
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/087098
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087208
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087609
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087759
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087827
PRIOR FILING DATE:	1998-06-03
PRIOR APPLICATION NUMBER:	60/088025
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088028
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088029
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088033
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088167
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088202
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PRIOR APPLICATION NUMBER:	60/088212
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088217
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088326
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088555
PRIOR FILING DATE:	1998-06-09
PRIOR APPLICATION NUMBER:	60/088722
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088738
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088740
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088811
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088824
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088825
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088826
PRIOR FILING DATE:	1998-06-10

[illegible]

Query Match	21.68;	Score 27.8;	DB 13;	Length 2037;
Best Local Similarity	57.58;	Pred. No. 5.1;		
Matches	50;	Mismatches	37;	Indels 0;
				Gaps 0;

42 ACANAAGACCCGACCGAGATGGTCGGGGCTTTTGTGTGGTGCTGTGACGTGTTGCC 101
| | | | | | | | | | | | | | | | | | | | | |
135 AAAAGACCATCATCTACATTGTCAGGGTCATTAAATCTTGTGTCGACTGTGGTTCCC 1276

102 AACCGTATTATTCGGACTAGTTCAGC 128
1275 CTGTTTGCATCTGGGACTAATGCATTC 1249

SSULT 10
-10-174-590-591/c
Sequence 591, Application US/10174590
Publication No. US20030008352A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P34301R1C42
 CURRENT APPLICATION NUMBER: US/10/174,590
 CURRENT FILING DATE: 2002-06-18
 Prior application removed - See File Wrapper or Palm
 Number of SEQ ID NOS: 612

SEQ ID NO 591
LENGTH: 2037
TYPE: DNA
ORGANISM: Homo Sapien
-10-174-590-591

Query Match	21.6%;	Score 27.8;	DB 14;	Length 2037;
Best Local Similarity	57.5%;	Pred. No. 5.1;		
Matches	50;	Conservative	0;	Mismatches 37;
			Indels	0;
			Gaps	0;

42 ACMAAGACCCGACCAGATGGTCGGGGCTTTTGTGTGGTGCTGTGACGTGTTGCC 101
| | | | | | | | | | | | | | | |
1335 AAAAAGACCATCTCAATTGCAGGGCACAATAATCGTTGGACACTGGGTTCCC 1276

102 AACCGTATTATCCGGACTAGTCAGC 128

Db 1275 CTGTTTGCATCTGGACTAATGCATC 1249

RESULT 11
US-10-176-758-591/c
; Sequence 591, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; ADDITIONAL PAGES: 2

APPLICANT:	Baker, Kevin E.
APPLICANT:	Chen, Jian
APPLICANT:	Desnoyers, Luc
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Gurney, Austin L.
APPLICANT:	Pen, James
APPLICANT:	Smith, Victoria
APPLICANT:	Watanabe, Colin K
APPLICANT:	Wood, William I.
APPLICANT:	Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACID POLYMERIZATION COMPOSITIONS
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: B3430R1C104
 CURRENT APPLICATION NUMBER: US/10/176,738
 CURRENT FILING DATE: 2002-06-21
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612

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; SEQ ID NO 591
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Homo Sapien
;
US-10-176-758-591

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Query Match	21.6%;	Score 27.8;	DB 14;	Length 2037;
Best Local Similarity	57.5%;	Pred. No. 5.1;		
Matches 50;	Conservative 0;	Mismatches 37;	Indels 0;	Gaps 0;

Ddb

OY		42	ACAAAGACC	C	GACCGAATGCTGGGTCTTTT	T	TGTCGTCGCCTGAACGTTTTGCC	101
	-		-	-	-		-	-
Db		1335	A AAAAGACA	TATCATTGTAAGG	SCTCACTAATCTGTTCCGACTGCGTTCCC	1276		

Qy	102	AACGTAATATTCGGACTAGTTCAGC	128
Db	1275	CTGTTGCTATCTGGGACTAATGCATC	1249

RESULT 12
US-10-175-737-591/c
; Sequence 591, Application US/10175737
; Publication No. US20030013153A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Collin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612

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; SEQ ID NO 591
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Homo Sapien

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US-10-175-737-591

Query Match 21.6%; Score 27.8; DB 14; Length 2037;

Best Local Similarity 57.5%; Pred. No. 5.1;

Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 42 ACAAGACCCCGACGAGATGTCGGGCTTTTGTGTGGTGTGACGTGTGTC 101

DB 1335 AAAAAGACCATCATCTACATTTGTACAGGTCATATATCTGTCTGACTGTGTTCC 1276

QY 102 AACCTATTATTCGGACTAGTTCAGC 128

DB 1275 CTGTTGCTATCTGGGACTAATGCAATC 1249

RESULT 13

US-10-173-706-591/c

Sequence 591, Application US/10173706

Publication No. US20030022293A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C7

CURRENT APPLICATION NUMBER: US/10/173,706

CURRENT FILING DATE: 2002-06-17

Prior Application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 591

LENGTH: 2037

TYPE: DNA

ORGANISM: Homo Sapien

US-10-173-706-591

Query Match 21.6%; Score 27.8; DB 14; Length 2037;

Best Local Similarity 57.5%; Pred. No. 5.1;

Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 42 ACAAGACCCCGACGAGATGTCGGGCTTTTGTGTGGTGTGACGTGTGTC 101

DB 1335 AAAAAGACCATCATCTACATTTGTACAGGTCATATATCTGTCTGACTGTGTTCC 1276

QY 102 AACCTATTATTCGGACTAGTTCAGC 128

DB 1275 CTGTTGCTATCTGGGACTAATGCAATC 1249

RESULT 14

US-10-175-738-591/c

Sequence 591, Application US/10175738

Publication No. US20030022294A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C45

CURRENT APPLICATION NUMBER: US/10/175,738

CURRENT FILING DATE: 2002-06-19

Prior Application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 591

LENGTH: 2037

TYPE: DNA

ORGANISM: Homo Sapien

US-10-175-738-591

Query Match 21.6%; Score 27.8; DB 14; Length 2037;

Best Local Similarity 57.5%; Pred. No. 5.1;

Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 42 ACAAGACCCCGACGAGATGTCGGGCTTTTGTGTGGTGTGACGTGTGTC 101

DB 1335 AAAAAGACCATCATCTACATTTGTACAGGTCATATATCTGTCTGACTGTGTTCC 1276

QY 102 AACCTATTATTCGGACTAGTTCAGC 128

DB 1275 CTGTTGCTATCTGGGACTAATGCAATC 1249

RESULT 15

US-10-175-752-591/c

Sequence 591, Application US/10175752

Publication No. US20030022295A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C60

CURRENT APPLICATION NUMBER: US/10/175,752

CURRENT FILING DATE: 2002-06-19

Prior Application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 591

LENGTH: 2037

TYPE: DNA

ORGANISM: Homo Sapien

US-10-175-752-591

Query Match 21.6%; Score 27.8; DB 14; Length 2037;

Best Local Similarity 57.5%; Pred. No. 5.1;

Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 42 ACAAGACCCCGACGAGATGTCGGGCTTTTGTGTGGTGTGACGTGTGTC 101

DB 1335 AAAAAGACCATCATCTACATTTGTACAGGTCATATATCTGTCTGACTGTGTTCC 1276

QY 102 AACCTATTATTCGGACTAGTTCAGC 128

DB 1275 CTGTTGCTATCTGGGACTAATGCAATC 1249

Search completed: August 25, 2003, 22:04:23

Job time : 50.5831 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:46:38 ; Search time 20.7296 Seconds
(without alignments)
2746.715 Million cell updates/sec

Title: US-09-816-391A-1_COPY_472_600

Perfect score: 129

Sequence: 1 tgaaccttcgcctcgtacgca.....tattccgactagttacgcy 129

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*

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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCUS.COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28.6	22.2	1146	US-09-252-991A-2602	Sequence 2602, Ap
2	28.6	22.2	2184	US-09-252-991A-2241	Sequence 2241, Ap
3	28.6	22.2	2868	US-09-252-991A-2311	Sequence 2311, Ap
4	28.4	22.0	14707	US-09-312-762A-3	Sequence 31, Appl
5	26.4	20.5	907	US-08-672-850-7	Sequence 7, Appl
6	26.2	20.3	907	US-08-672-850-11	Sequence 11, Appl
7	26.2	20.3	907	US-09-565-177A-7	Sequence 7, Appl
8	26.2	20.3	907	US-09-565-177A-11	Sequence 11, Appl
9	26.2	20.3	1001	US-08-672-850-10	Sequence 10, Appl
10	26.2	20.3	1001	US-09-565-177A-10	Sequence 10, Appl
11	26.2	20.3	1074	US-08-804-227C-1	Sequence 7, Appl
12	26.2	20.3	1158	US-09-198-092-1	Sequence 1, Appl
13	25.8	20.0	2262	US-08-674-887A-5	Sequence 5, Appl
14	25.8	20.0	2262	US-08-951-844-5	Sequence 5, Appl
15	25.8	20.0	2262	US-09-412-347-5	Sequence 5, Appl
16	25.8	20.0	2271	US-09-313-284A-1215	Sequence 1215, Ap
17	25.6	19.8	1586	US-08-461-244-1	Sequence 1, Appl
18	25.4	19.7	1586	US-09-016-434-1096	Sequence 1096, Ap
19	25.4	19.7	30302	US-09-221-017B-174	Sequence 174, Appl
20	25.4	19.7	50341	US-08-247-901C-1	Sequence 1, Appl
21	25.2	19.5	50341	US-09-075-904-1	Sequence 1, Appl
22	25.2	19.5	52297	US-08-426-436-1	Sequence 1, Appl
23	25.2	19.5	52297	US-08-705-357-1	Sequence 1, Appl
24	25.2	19.5	52297	US-09-634-238-120	Sequence 120, Appl
25	25.2	19.4	3613	US-08-483-101-1	Sequence 1, Appl
26	25.2	19.4	5798	US-08-483-101-1	Sequence 1, Appl
27	25.2	19.4	5798	US-08-483-101-1	Sequence 1, Appl

28	24.8	19.2	799	1	US-08-173-510B-100	Sequence 100, Appl
29	24.8	19.2	799	1	US-08-458-218-98	Sequence 98, Appl
30	24.8	19.2	799	2	US-08-450-497-100	Sequence 100, Appl
31	24.8	19.2	942	4	US-09-134-001C-2784	Sequence 2784, Appl
32	24.8	19.2	4067	4	US-08-894-454-164	Sequence 164, Appl
33	24.6	19.1	612	4	US-09-252-991A-2454	Sequence 2454, Appl
34	24.6	19.1	678	4	US-09-252-991A-2221	Sequence 2221, Appl
35	24.6	19.1	753	4	US-09-252-991A-2382	Sequence 2382, Appl
36	24.6	19.1	2814	4	US-09-252-991A-2537	Sequence 2537, Appl
37	24.6	19.1	4670	4	US-09-700-971-2	Sequence 2, Appl
38	24.4	18.9	801	4	US-09-252-991A-5148	Sequence 5148, Appl
39	24.4	18.9	1269	4	US-09-252-991A-5037	Sequence 5037, Appl
40	24.4	18.9	2031	4	US-09-252-991A-5180	Sequence 5180, Appl
41	24.4	18.9	1830121	4	US-09-557-884-1	Sequence 1, Appl
42	24.4	18.9	1830121	4	US-09-643-990A-1	Sequence 1, Appl
43	24.4	18.8	639	4	US-09-252-991A-2342	Sequence 2342, Appl
44	24.2	18.8	1047	4	US-09-252-991A-11024	Sequence 11024, A
45	24.2	18.8	1092	4	US-09-252-991A-11235	Sequence 11235, A

ALIGNMENTS

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RESULT 1
US-09-252-991A-2602/c
Sequence 2602, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2602
LENGTH: 1146
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2602

Query Match          22.2%; Score 28.6; DB 4; Length 1146;
Best Local Similarity 57.1%; Pred. No. 0.61;
Matches 52; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 39 ACGACAAAGACCCCGACGAGATGTCGGGCTCTTTTGTGTGTCGTCTGTGACGTGTG 98
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 906 ACGATCAAGACCCCGACGAGATGTCGGGCTCTTTTGTGTGTCGTCTGTGACGTGTG 847
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 99 TCCAACCGTATTTATTCGCGACTAGTTCAGCG 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 846 TTGAGCTGGCGCAAGCTCTTCAGGTGCGG 816
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
US-09-252-991A-2241
Sequence 2241, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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```

; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey
; APPLICANT: Araki, Toshiyuki
; TITLE OF INVENTION: NINJURIN

```

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QY      71 CTTTTCGTTGCGTCTG  89
          |||||  |||  ||
Db      468 GTTGTGAGCTGGTTGAGT  450

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RESULT 12
US-09-934-901-7/c
Sequence 7, Application US/09934901
Patent No. 655353
GENERAL INFORMATION:
APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: No. 655353ton, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: C1619 US NA
CURRENT APPLICATION NUMBER: US/09/934,901
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,906
PRIOR FILING DATE: September 1, 2000
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
LENGTH: 1074
TYPE: DNA
ORGANISM: METHYLOMONAS SP.
US-09-934-901-7

Query Match 20.2%; Score 26; DB 4; Length 1074;
Best Local Similarity 62.1%; Pred. No. 5.3;
Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 37 TGACGACAAAGACCCGACGAGATGCTTTTGTGTGCTGTGACGTGT 96
DB 670 TGCAGAAAGACCCGACGAGATGCTTTTGTGTGCTGTGACGTGT 96
Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 97 TGTCCA 102
DB 610 AAGCCA 605

RESULT 13
US-08-804-227C-1/c
Sequence 1, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: Dehoff, Bradley S.
APPLICANT: Kuhlthoss, Stuart A.
APPLICANT: Kosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 43280 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 816..14234
FEATURE:
NAME/KEY: CDS
LOCATION: 14351..19945
FEATURE:
NAME/KEY: CDS
LOCATION: 20010..31199
FEATURE:
NAME/KEY: CDS
LOCATION: 31232..36067
FEATURE:
NAME/KEY: CDS
LOCATION: 36249..41774
US-08-804-227C-1

Query Match 20.2%; Score 26; DB 2; Length 43280;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 38 GAGGACAAAGACCCGACGAGATGCTTTTGTGTGCTGTGACGTGT 97
DB 13262 GACCGGACAAAGACCCGACGAGATGCTTTTGTGTGCTGTGACGTGT 13203
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 98 GTCAACCGCTATTATTCGCGACTAGTTTCAG 127
DB 13202 CGCCTTCGCGCGCATGACGTACCAGATCCG 13173

RESULT 14
US-09-198-092-1/c
Sequence 1, Application US/09198092A
Patent No. 6214575
GENERAL INFORMATION:
APPLICANT: Yano, Masamitsu
APPLICANT: Omura, Mitsuo
APPLICANT: Ikoma, Yoshiro
APPLICANT: Komatsu, Akira
TITLE OF INVENTION: BETA-CAROTENE HYDROXYLASE GENE
FILE REFERENCE: 07898/033001
CURRENT APPLICATION NUMBER: US/09/198,092A
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: JP97/331936
EARLIER FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1158
TYPE: DNA
ORGANISM: Citrus unshiu
FEATURE:
NAME/KEY: CDS
LOCATION: (87)..(1019)
US-09-198-092-1

Query Match 20.0%; Score 25.8; DB 3; Length 1158;
Best Local Similarity 63.9%; Pred. No. 6.5;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 37 TGACGACAAAGACCCGACGAGATGCTTTTGTGTGCTGTGACGTGT 96
DB 111 TGCAGAAAGACCCGACGAGATGCTTTTGTGTGCTGTGACGTGT 52
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 97 T 97
DB 51 T 51

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:56:32 ; Search time 73.798 Seconds
(without alignments)
5849.036 Million cell updates/sec

Title: US-09-816-391A-1_COPY_1_192

Perfect score: 192
Sequence: 1 gctggcgccgagcgcacatga.....tgaccacagaagatgctt 192

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCF_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 6: /cgn2_6/ptodata/2/pubpna/PCFUS_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	100.0	600	US-09-816-391A-1	Sequence 1, Appl1
2	33.2	17.3	824	US-10-027-632-167810	Sequence 167810,
3	32.4	16.9	484	US-10-027-632-6585	Sequence 6585, Ap
4	31.2	16.2	18372	US-09-764-891-8869	Sequence 8869, Ap
5	30.6	15.9	1099	US-10-027-632-10536	Sequence 10536, A
6	30.2	15.7	515	US-09-864-761-16206	Sequence 16206, A
7	30	15.6	639	US-10-027-632-18596	Sequence 18596,
8	29.8	15.5	501	US-10-027-632-270844	Sequence 270844,
9	29.6	15.4	453	US-10-027-632-266872	Sequence 266872,
10	29.4	15.3	487	US-09-918-995-12674	Sequence 12674, A
11	29.4	15.3	614	US-10-027-632-221811	Sequence 221811,
12	29.4	15.3	507	US-09-766-632-221812	Sequence 221812,
13	29.2	15.2	507	US-10-040-862-4795	Sequence 4795, Ap
14	29.2	15.2	507	US-10-027-632-97328	Sequence 97328, A
15	29.2	15.2	1712	US-10-027-632-97329	Sequence 97329, A
16	29.2	15.2	1712	US-10-027-632-97329	Sequence 97329, A

17	29.2	15.2	2190	14	US-10-217-371-5	Sequence 5, Appl1
18	29.2	15.2	2250	14	US-10-217-371-13	Sequence 13, Appl1
19	29.2	15.2	2253	14	US-10-217-371-3	Sequence 3, Appl1
20	29.2	15.2	2274	14	US-10-217-371-9	Sequence 9, Appl1
21	29.2	15.2	2313	14	US-10-217-371-11	Sequence 11, Appl1
22	29.2	15.2	2337	14	US-10-217-371-7	Sequence 7, Appl1
23	29.2	15.2	2508	14	US-10-176-847-45	Sequence 45, Appl1
24	29.2	15.2	2937	14	US-10-176-847-45	Sequence 150, App
25	29.2	15.2	3077	12	US-10-301-822-150	Sequence 179, App
26	29.2	15.2	3077	14	US-10-171-311-179	Sequence 471, App
27	29.2	15.2	3202	9	US-09-925-301-471	Sequence 148, App
28	29.2	15.2	3213	12	US-10-301-822-148	Sequence 32, Appl1
29	29.2	15.2	3213	12	US-10-304-752-32	Sequence 177, App
30	29.2	15.2	3213	14	US-10-171-311-177	Sequence 341, App
31	29.2	15.2	3213	14	US-10-177-293-341	Sequence 9861, Ap
32	29.2	15.2	3681	14	US-10-198-846-9861	Sequence 193, App
33	29.2	15.2	6465	10	US-09-954-456-193	Sequence 1319, Ap
34	29.2	15.1	1444	14	US-10-106-698-1319	Sequence 1, Appl1
35	29.2	15.1	1830121	14	US-10-329-960-1	Sequence 2315, Ap
36	28.8	15.0	413	10	US-09-867-701-2315	Sequence 663, App
37	28.8	15.0	419	10	US-09-783-590-663	Sequence 20927, App
38	28.8	15.0	611	13	US-10-027-632-209927	Sequence 20928, App
39	28.8	15.0	611	13	US-10-027-632-209928	Sequence 20929, App
40	28.8	15.0	611	13	US-10-027-632-209929	Sequence 20930, App
41	28.8	15.0	611	13	US-10-027-632-209930	Sequence 160356, App
42	28.8	15.0	835	13	US-10-027-632-160356	Sequence 3770, App
43	28.4	14.8	345	10	US-09-974-300-3770	Sequence 243, App
44	28.4	14.8	75899	9	US-09-854-883-243	Sequence 413, App
45	28.2	14.7	279	12	US-10-238-075-413	

ALIGNMENTS

RESULT 1
US-09-816-391A-1
Sequence 1, Application US/09816391A
Patent No. US20020054865A1
GENERAL INFORMATION:
APPLICANT: FUJIMORI, Minoru
APPLICANT: TANIGUCHI, Shunichiro
APPLICANT: AMANO, Jun
APPLICANT: YAZAWA, Kazuyuki
APPLICANT: KANO, Yasunobu
APPLICANT: NAKAMURA, Toshiyuki
APPLICANT: SASAKI, Takayuki
TITLE OF INVENTION: Anaerobic bacterium as a drug for cancer gene therapy
FILE REFERENCE: 2001-WMC/01736
CURRENT APPLICATION NUMBER: US/09/816,391A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 00/287688
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 1
LENGTH: 600
TYPE: DNA
ORGANISM: Bifidobacterium longum
FEATURE:
NAME/KEY: CDS
LOCATION: (193)..(471)
US-09-816-391A-1

Query Match 100.0%; Score 192; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 7.2e-55;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCTGGCGCCGCGGCACGAGTGGCTTGACAGCATATCTGTCATTCGCTATTT 60
1 GCTGGCGCCGCGGCACGAGTGGCTTGACAGCATATCTGTCATTCGCTATTT 60
61 TCAATACCTTGGGGGAATAGATGGAACCCCTATATAACCGGGGTTTCGCAAAAC 120
61 TCAATACCTTGGGGGAATAGATGGAACCCCTATATAACCGGGGTTTCGCAAAAC 120

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OY 121 ATGGCTAGTATCATGATGACATGACATGACAAAGTCGTCGCTGACCCCA 180
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
DB 121 ATGGCTAGTATCATGATGACATGACATGACAAAGTCGTCGCTGACCCCA 180
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
OY 181 GAAGATGCTTT 192
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
DB 181 GAAGATGCTTT 192
; SEQ ID NO: 6585
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-6585

RESULT 2
US-10-027-632-167810/c
; Sequence 167810, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 167810
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-167810

Query Match
Best Local Similarity 17.3%; Score 33.2; DB 13; Length 824;
Matches 56; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 76 AATGATGTGAAAACCCCTATATAAACGCGGTTTCGAGAAACATGCGCTAGTTCAT 135
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
DB 384 AATGATGTGAAAACCCCTATATAAACGCGGTTTCGAGAAACATGCGCTAGTTCAT 135
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
OY 136 TGATGACATGACTAGTAAAGTGGCTGTC 169
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
DB 324 TGATGACATGACTAGTAAAGTGGCTGTC 291
; SEQ ID NO: 8869
; LENGTH: 18272
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8869

Query Match
Best Local Similarity 16.2%; Score 31.2; DB 11; Length 18272;
Matches 51; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 71 CGGGGAATAGATGTAAGAAACCCCTATATAAACGCGGTTTCGAGAAACATGCGCTAGT 130
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
DB 17088 CGGGGAATAGATGTAAGAAACCCCTATATAAACGCGGTTTCGAGAAACATGCGCTAGT 130
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
OY 131 ATCATTGATGACACATGACTAA 154
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
DB 17028 ATCATTGATGACACATGACTAA 154
; SEQ ID NO: 8869
; LENGTH: 18272
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8869

Query Match
Best Local Similarity 16.9%; Score 32.4; DB 13; Length 484;
Matches 51; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

OY 36 ATATCTGTCTGATGCTCTATTTTCATATCTTCGAGAAATAGATGAAACCTT 95
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
DB 130 ATATCTGTCTGATGCTCTATTTTCATATCTTCGAGAAATAGATGAAACCTT 95
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
OY 96 ATAAACGCGGTTTCGACAAA 119
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
DB 190 ATAAACGCGGTTTCGACAAA 213
; SEQ ID NO: 8869
; LENGTH: 18272
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8869

RESULT 4
US-09-764-891-8869/c
; Sequence 8869, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 8869
; LENGTH: 18272
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8869

Query Match
Best Local Similarity 60.7%; Score 32.4; DB 13; Length 484;
Matches 51; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

OY 36 ATATCTGTCTGATGCTCTATTTTCATATCTTCGAGAAATAGATGAAACCTT 95
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
DB 130 ATATCTGTCTGATGCTCTATTTTCATATCTTCGAGAAATAGATGAAACCTT 95
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
OY 96 ATAAACGCGGTTTCGACAAA 119
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
DB 190 ATAAACGCGGTTTCGACAAA 213
; SEQ ID NO: 8869
; LENGTH: 18272
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8869

RESULT 5
US-10-027-632-10536/c
; Sequence 10536, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
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; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 6585
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-6585

Query Match
Best Local Similarity 16.9%; Score 32.4; DB 13; Length 484;
Matches 51; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

OY 36 ATATCTGTCTGATGCTCTATTTTCATATCTTCGAGAAATAGATGAAACCTT 95
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
DB 130 ATATCTGTCTGATGCTCTATTTTCATATCTTCGAGAAATAGATGAAACCTT 95
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
OY 96 ATAAACGCGGTTTCGACAAA 119
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
DB 190 ATAAACGCGGTTTCGACAAA 213
; SEQ ID NO: 8869
; LENGTH: 18272
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8869

RESULT 4
US-09-764-891-8869/c
; Sequence 8869, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 8869
; LENGTH: 18272
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8869

Query Match
Best Local Similarity 16.2%; Score 31.2; DB 11; Length 18272;
Matches 51; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 71 CGGGGAATAGATGTAAGAAACCCCTATATAAACGCGGTTTCGAGAAACATGCGCTAGT 130
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
DB 17088 CGGGGAATAGATGTAAGAAACCCCTATATAAACGCGGTTTCGAGAAACATGCGCTAGT 130
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
OY 131 ATCATTGATGACACATGACTAA 154
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
DB 17028 ATCATTGATGACACATGACTAA 154
; SEQ ID NO: 8869
; LENGTH: 18272
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8869

Query Match
Best Local Similarity 16.9%; Score 32.4; DB 13; Length 484;
Matches 51; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

OY 36 ATATCTGTCTGATGCTCTATTTTCATATCTTCGAGAAATAGATGAAACCTT 95
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
DB 130 ATATCTGTCTGATGCTCTATTTTCATATCTTCGAGAAATAGATGAAACCTT 95
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
OY 96 ATAAACGCGGTTTCGACAAA 119
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
DB 190 ATAAACGCGGTTTCGACAAA 213
; SEQ ID NO: 8869
; LENGTH: 18272
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8869

RESULT 5
US-10-027-632-10536/c
; Sequence 10536, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10536
LENGTH: 1099
TYPE: DNA
ORGANISM: Human
US-10-027-632-10536

Query Match 15.9%; Score 30.6; DB 13; Length 1099;
Best Local Similarity 50.3%; Pred. No. 5.4;
Matches 75; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 35 CATATCTGTGTCGATTCGTATTTTCATACCTTCGGGGAATAGATGTGAACCCCT 94
DB 202 CATGTTTATTTAAATGAGACTTTTCAAAACCTGTGTGTTTATATACCAACATA 143
QY 95 TTTAAACGGGGTTTCCGACAAACATGCGCTAGTATCATTTGACACATGACCTAA 154
DB 142 AATTGAAAACGACCTTACACGACATTAAGATGACGATTAATATTAACATGAATA 83
QY 155 GCAAAAGTCCTGTCCTCCCTGACCCAGAA 183
DB 82 TTTAAATGTTCGCCATTTACCCATGTA 54

RESULT 6
US-09-864-761-16206
Sequence 16206, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 16206
LENGTH: 515
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC00062.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
US-09-864-761-16206

Query Match 15.7%; Score 30.2; DB 9; Length 515;
Best Local Similarity 49.7%; Pred. No. 5.1;
Matches 77; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 13 GCCCATGAAGTGGCTGACACATATCTGTCGATTCGTCCTATTTTCATACCTTG 72
DB 253 GCCCTTAAATATACGATGATATTTATTTAGTACGATGAGTGTAAATCTTTAA 312
QY 73 GGAATATAGATGTGAATAACCTTATTAACGCGGGTTTCCGCAACATGCGCTAGTAT 132
DB 313 TAGAAGTAGATGATAGATCAATTCACATTAATGTTTATGATGATATCATGCTGTTT 372
QY 133 CATGATGACACATGACGACTAGCAAAAGTCTTG 167
DB 373 GTTTACTGCTCTTAAACTTTTGAACCTGCTG 407

RESULT 7
US-10-027-632-185956/C
Sequence 185956, Application US/10027632
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 185956
LENGTH: 639
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(639)


```
; Sequence 221811, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221811
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-221811

Query Match      15.3%  Score 29.4;  DB 13;  Length 614;
Best Local Similarity 52.0%;  Pred. No. 10;
Matches 66;  Conservative 0;  Mismatches 61;  Indels 0;  Gaps 0;

OY      55 CATTTCATACCTCGGGGAATGATGTGAAACCCCTATATAACGGGGTTTCGC 114
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      291 CTAAGCTTTTCACTCTTAAATAATGTCAAATCTGTTGAAAAGAAATATATGC 232
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      115 AGAAACATGCGGTAGTATCTTGTATGACACATGAGCTAAGCAAAAGTGTGCCCCCTG 174
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      231 ATAAATATAAAACATACAAACATATATAAATGAAATGTTAAATGCTTCTCTCTG 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      175 ACCCAAG 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      171 TCTTCAG 165
```

```
; SEQ ID NO 221812
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-221812

Query Match      15.3%  Score 29.4;  DB 13;  Length 614;
Best Local Similarity 52.0%;  Pred. No. 10;
Matches 66;  Conservative 0;  Mismatches 61;  Indels 0;  Gaps 0;

OY      55 CATTTCATACCTCGGGGAATGATGTGAAACCCCTATATAACGGGGTTTCGC 114
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      291 CTAAGCTTTTCACTCTTAAATAATGTCAAATCTGTTGAAAAGAAATATATGC 232
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      115 AGAAACATGCGGTAGTATCTTGTATGACACATGAGCTAAGCAAAAGTGTGCCCCCTG 174
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      231 ATAAATATAAAACATACAAACATATATAAATGAAATGTTAAATGCTTCTCTCTG 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      175 ACCCAAG 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      171 TCTTCAG 165

RESULT 13
US-09-796-692-4795
; Sequence 4795, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE OF INVENTION: HEPAATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4795
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-4795

Query Match      15.2%  Score 29.2;  DB 10;  Length 507;
Best Local Similarity 59.8%;  Pred. No. 11;
Matches 49;  Conservative 0;  Mismatches 33;  Indels 0;  Gaps 0;

OY      89 AACCTATAAACGGCGGTTTCGACGAAACATGCGCTAGTATCATGTATGACACATG 148
```

b 339 AACCATATCTAATGGGCTGTCACTTAATGTGCTCAATCATCCATGGAACCA 398
y 149 GACTAAGCAAAAGTCTGTCC 170
b 399 ATTGCAACAATATGCTGTGTCC 420

ESULT 14

S-10-040-862-4795.
Sequence 4795, Application US/10040862
Publication No. US20030078396A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4795

LENGTH: 507
TYPE: DNA
ORGANISM: Homo sapiens
S-10-040-862-4795

Query Match 15.2%; Score 29.2; DB 14; Length 507;
Best Local Similarity 59.8%; Pred. No. 11;
Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

y 89 AACCTTATTAACCGGGGTTTCAGAAACATCGCTAGATCATGATGACAACATG 148
|||||
b 339 AACCTTATCTAATGGGCTGTCACTTAATGTGCTCAATCATCCATGGAACCA 398
y 149 GACTAAGCAAAAGTCTGTCC 170
|||||
b 399 ATTGCAACAATATGCTGTGTCC 420

ESULT 15
S-10-027-632-97328
Sequence 97328, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827,129
CURRENT FILING DATE: US/10/027,632
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97328
LENGTH: 1712
TYPE: DNA
ORGANISM: Human
S-10-027-632-97328

Query Match 15.2%; Score 29.2; DB 13; Length 1712;
Best Local Similarity 48.8%; Pred. No. 20;
Matches 79; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

y 20 AAGTGGCTTGACAAGCATATATCTGTGATTCGCTATTTCAATACCTTCGGGGAAT 79
|||||
b 1490 AAGTGGCTCTTAAGGATATCTAGCTACAGTTGCTAGAAATTTCTTGATGAAGTT 1549
y 80 AGATGTGAACCCCTTTPAAGCGGGTTTCAGAAACATGCGTATGATCATGAT 139
|||||
b 1550 AGAAGCTAGATTTCTACAGATATCTCCAGAGAGGACATTTGTAAAGCATTTAT 1609
y 140 GACAACATGACTAAGCAAAAGTCTGTCCCTGACCCCAAG 181
|||||
b 1610 TACACTGGTGGGAGGCGACATCTGCTCTGTTCAAG 1651

Search completed: August 25, 2003, 22:04:22
Job time : 76.798 secs


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c 5 34.6 18.0 425 30 US-09-684-016-322494 Sequence 322494,
6 34 17.7 180220 75 US-60-212-664-193 Sequence 193, App
7 34 17.7 6853926 40 US-09-947-916-137 Sequence 137, App
8 33.4 17.4 589 27 US-09-637-890-992 Sequence 992, App
9 33.4 17.4 50000 22 US-09-513-647B-11 Sequence 11, App
c 10 33.4 17.4 2420479 40 US-09-947-911-305 Sequence 305, App
c 11 33.2 17.3 824 27 US-09-634-306B-167810 Sequence 167810,
c 12 33.2 17.3 824 27 US-10-027-632-422-55 Sequence 167810,
c 13 33.2 17.3 32768 74 US-60-207-422-55 Sequence 55, App1
c 14 33.2 17.3 133318 22 US-09-528-237A-20 Sequence 20, App1
c 15 32.8 17.1 12360069 40 US-09-948-128-318 Sequence 318, App
c 16 32.6 17.0 2570 22 US-09-513-999C-31601 Sequence 31601, App
c 17 32.6 17.0 2570 91 US-10-144-771-6009 Sequence 6009, App
c 18 32.6 17.0 2570 91 US-60-360-207-6009 Sequence 6009, App
c 19 32.4 16.9 484 27 US-09-634-306B-6585 Sequence 6585, App
c 20 32.4 16.9 484 27 US-10-027-632-6585 Sequence 6585, App
c 21 32.4 16.9 2717 26 US-09-614-150-30178 Sequence 30178, App
c 22 32.4 16.9 2717 26 US-09-191-637-29726 Sequence 29726, App
c 23 32.4 16.9 74172 22 US-09-528-237A-921 Sequence 921, App
c 24 32.4 16.9 1160003 40 US-09-947-911-238 Sequence 238, App
c 25 32.2 16.8 525 35 US-09-834-366-9232 Sequence 9232, App
c 26 32.2 16.8 525 73 US-60-197-873-9232 Sequence 9232, App
c 27 32 16.7 495269 51 US-60-252-833-30435 Sequence 30435, App
c 28 32 16.7 3011308 51 US-10-398-221-8 Sequence 8, App1
c 29 32 16.7 3011308 51 US-09-398-221-2058 Sequence 2058, App
c 30 31.8 16.6 398 30 US-09-699-999-3551 Sequence 3551, App
c 31 31.8 16.6 175847 35 US-09-855-768-18 Sequence 18, App1
c 32 31.8 16.6 1059516 40 US-09-947-911-86 Sequence 86, App1
c 33 31.6 16.5 438 20 US-09-394-745-12555 Sequence 12555, App
c 34 31.6 16.5 438 25 US-09-565-306-32998 Sequence 32998, App
c 35 31.6 16.5 670 74 US-09-865-439A-59941 Sequence 59941, App
c 36 31.6 16.5 670 74 US-60-207-458-104101 Sequence 104101, App
c 37 31.6 16.5 1878 28 US-09-654-617-261052 Sequence 261052, App
c 38 31.6 16.5 1878 28 US-09-684-016-261052 Sequence 261052, App
c 39 31.4 16.4 384 19 US-09-304-517A-91809 Sequence 91809, App
c 40 31.4 16.4 384 20 US-09-394-745-19452 Sequence 19452, App
c 41 31.4 16.4 384 25 US-09-565-306-42940 Sequence 42940, App
c 42 31.4 16.4 384 25 US-09-985-678-91809 Sequence 91809, App
c 43 31.4 16.4 501 20 US-09-371-146A-91809 Sequence 91809, App
c 44 31.4 16.4 161812 22 US-09-528-237A-1697 Sequence 1697, App
c 45 31.2 16.2 140 28 US-09-654-617-87312 Sequence 87312, App

```

ALIGNMENTS

RESULT 1

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US-09-816-391a-1
: Sequence 1, Application US/09816391A
: GENERAL INFORMATION:
: APPLICANT: FUJIMORI, Minoru
: APPLICANT: TANIGUCHI, Shunichihiro
: APPLICANT: AMANO, Jun
: APPLICANT: YAZAWA, Kazuyuki
: APPLICANT: KANO, Yasunobu
: APPLICANT: NAKAMURA, Toshiyuki
: APPLICANT: SASAKI, Takayuki
: TITLE OF INVENTION: Anaerobic bacterium as a drug for cancer gene therapy
: FILE REFERENCE: 2001-WK/01736
: CURRENT APPLICATION NUMBER: US/09/816, 391A
: PRIOR FILING DATE: 2001-03-26
: PRIOR FILING DATE: 2000-09-21
: NUMBER OF SEQ ID NOS: 3
: SEQ ID NO 1
: LENGTH: 600
: TYPE: DNA
: ORGANISM: Bifidobacterium longum
: NAME/KEY: CDS
: LOCATION: (193)..(471)
: US-09-816-391a-1

```

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Sequence 322494,
Sequence 193, App
Sequence 137, App
Sequence 992, App
Sequence 11, App1
Sequence 305, App
Sequence 167810,
Sequence 167810,
Sequence 55, App1
Sequence 20, App1
Sequence 318, App
Sequence 31601, App
Sequence 6009, App
Sequence 6009, App
Sequence 6585, App
Sequence 6585, App
Sequence 30178, App
Sequence 29726, App
Sequence 921, App
Sequence 238, App
Sequence 9232, App
Sequence 9232, App
Sequence 30435, App
Sequence 8, App1
Sequence 2058, App
Sequence 3551, App
Sequence 18, App1
Sequence 86, App1
Sequence 12555, App
Sequence 32998, App
Sequence 59941, App
Sequence 104101, App
Sequence 261052, App
Sequence 261052, App
Sequence 91809, App
Sequence 19452, App
Sequence 42940, App
Sequence 91809, App
Sequence 91809, App
Sequence 1697, App
Sequence 87312, App

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Query Match 100.0%; Score 192; DB 34; Length 600;
Best Local Similarity 100.0%; Pred. No. 4e-51;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGGGGGGGGGCCATGATGGTTCGACAGCAATATCTGTGATGATCTTATTT
DB 1 GCTGGGGGGGGGGCCATGATGGTTCGACAGCAATATCTGTGATGATCTTATTT
QY 61 TCATACCTTCGGGGGAATATGATGTGAACCCCTATTAACCGGGTTTCGAGAAC
DB 61 TCATACCTTCGGGGGAATATGATGTGAACCCCTATTAACCGGGTTTCGAGAAC
QY 121 ATCCGCTAGATATGATGATGACACATGACTAGCAAAAGTCTTGTCCCTGACCCAA
DB 121 ATCCGCTAGATATGATGATGACACATGACTAGCAAAAGTCTTGTCCCTGACCCAA
QY 181 GAAGATGCTTT 192
DB 181 GAAGATGCTTT 192

```

RESULT 2

```

US-09-394-745-18867/c
: Sequence 18867, Application US/09394745
: GENERAL INFORMATION:
: APPLICANT: Fisher, Dane K.
: APPLICANT: Laljudi, Raghuath V.
: TITLE OF INVENTION: NOCLETIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI
: FILE REFERENCE: 38-21(115454)B
: CURRENT APPLICATION NUMBER: US/09/394, 745
: CURRENT FILING DATE: 1999-09-15
: NUMBER OF SEQ ID NOS: 57264
: SEQ ID NO 18867
: LENGTH: 425
: TYPE: DNA
: ORGANISM: Zea mays
: OTHER INFORMATION: Clone ID: LIB3062-017-Q1-K1-C7
: US-09-394-745-18867

```

```

Query Match 18.0%; Score 34.6; DB 20; Length 425;
Best Local Similarity 51.6%; Pred. No. 3.6;
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

```

```

QY 16 CATGAGTGGCTGACAGCATATCTGCTATTCGCTATTTCAATCCTGCGG 75
DB 187 CTGAATCTGACGACAGATTAAGCTAATTTTCACCCAAACAAATGATATATGC 128
QY 76 AATAGATGTGAACCCCTTAATAACGCGGTTTCGAGAAACATGCGCTAGTATCAT 135
DB 127 AATGACGCAATTAATCATTTGAATGCTATTTACATATATCAAGACACTGTAAGT 68
QY 136 TGATGACACATGACTAGCAAAAGTCTGT 168
DB 67 TACTGCCACAAATAGCTAAACAGAGAGGTGT 35

```

RESULT 3

```

US-09-565-306-42355/c
: Sequence 42355, Application US/09565306
: GENERAL INFORMATION:
: APPLICANT: Andersen, Scott E.
: APPLICANT: Conner, Timothy W.
: APPLICANT: Laljudi, Raghuath V.
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated wi
: FILE REFERENCE: 38-21(115459)C
: CURRENT APPLICATION NUMBER: US/09/565, 306
: CURRENT FILING DATE: 2000-05-04
: NUMBER OF SEQ ID NOS: 83523
: SEQ ID NO 42355
: LENGTH: 425
: TYPE: DNA

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ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: LIB3062-017-Q1-K1-C7
US-09-565-306-42355

Query Match 18.0%; Score 34.6; DB 25; Length 425;
Best Local Similarity 51.6%; Pred. No. 3.6;
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

16 CAGGAAGTGGCTTGACAGACATATCTGTCTGATTCGTCTATTTCATATACCTCGGG 75
187 CTGGAATCTACGACCAAGATAGACTAAATTTTCCACCAAAACAAATCTAATATGC 128
76 AATAGATGTGAAAACCCCTATATAACGCGGTTTTCGAGAAACATGCGCTAGTATCAT 135
127 AATGACGCAATTAATCATTTTGAATGCGCTATTATACATATACAAAGCACTGCTAGACT 68
136 TGATGACACATGAGCTATACGAAAAGTGCCTGT 168
67 TACTGCCACAAATAGCTTAACAGAAAGGTGT 35

RESULT 4
US-09-654-617-322494/c
Sequence 322494, Application US/09654617
GENERAL INFORMATION:

APPLICANT: Liu, Jinsong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 322494
LENGTH: 425
TYPE: DNA
ORGANISM: Zea mays

US-09-654-617-322494

Query Match 18.0%; Score 34.6; DB 28; Length 425;
Best Local Similarity 51.6%; Pred. No. 3.6;
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

16 CAGGAAGTGGCTTGACAGACATATCTGTCTGATTCGTCTATTTCATATACCTCGGG 75
187 CTGGAATCTACGACCAAGATAGACTAAATTTTCCACCAAAACAAATCTAATATGC 128
76 AATAGATGTGAAAACCCCTATATAACGCGGTTTTCGAGAAACATGCGCTAGTATCAT 135
127 AATGACGCAATTAATCATTTTGAATGCGCTATTATACATATACAAAGCACTGCTAGACT 68
136 TGATGACACATGAGCTATACGAAAAGTGCCTGT 168
67 TACTGCCACAAATAGCTTAACAGAAAGGTGT 35

RESULT 5

US-09-684-016-322494/c
Sequence 322494, Application US/09684016
GENERAL INFORMATION:

APPLICANT: Kovalic, David K.
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654,617
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 322494
LENGTH: 425
TYPE: DNA
ORGANISM: Zea mays

US-09-684-016-322494

Query Match 18.0%; Score 34.6; DB 30; Length 425;
Best Local Similarity 51.6%; Pred. No. 3.6;
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

16 CAGGAAGTGGCTTGACAGACATATCTGTCTGATTCGTCTATTTCATATACCTCGGG 75
187 CTGGAATCTACGACCAAGATAGACTAAATTTTCCACCAAAACAAATCTAATATGC 128
76 AATAGATGTGAAAACCCCTATATAACGCGGTTTTCGAGAAACATGCGCTAGTATCAT 135
127 AATGACGCAATTAATCATTTTGAATGCGCTATTATACATATACAAAGCACTGCTAGACT 68
136 TGATGACACATGAGCTATACGAAAAGTGCCTGT 168
67 TACTGCCACAAATAGCTTAACAGAAAGGTGT 35

RESULT 6
US-60-212-664-193
Sequence 193, Application US/60212664
GENERAL INFORMATION:

APPLICANT: Ladunga, Steve
APPLICANT: Spier, Gene
APPLICANT: Greenberg, Simon
APPLICANT: Radkin, Steven
APPLICANT: Wang, Yu
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
FILE REFERENCE: C1000687
CURRENT APPLICATION NUMBER: US/60/212,664
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 636
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 193
LENGTH: 180220
TYPE: DNA
ORGANISM: HUMAN

FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(180220)
OTHER INFORMATION: n = A,T,C or G
US-60-212-664-193

Query Match 17.7%; Score 34; DB 75; Length 180220;
Best Local Similarity 54.9%; Pred. No. 40;
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

43 TGTCTGATTCGTCTATTTCATATACCTTCGGGGAATAGATGGAACCCCTATATAAC 102
128795 TGTATATTTGACTCTATTTAAATCTTCAGAAAAATTAACGACACACTTATTTACAA 128854
103 GCGGGTTTTCGAGAAACATGCGCTAGTATCATGATGACACATGAGCTAAGCAAAAGT 162
128855 GTTTTTCGAAATTAATAAAGCTTAGAACATTTTATATAAAGTAAAGTAAATTAAT 128914
163 GC 164
128915 TC 128916

RESULT 7

US-09-947-916-137
Sequence 137, Application US/09947916
GENERAL INFORMATION:

APPLICANT: Venter, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON
FILE REFERENCE: C1001296
CURRENT APPLICATION NUMBER: US/09/947,916
CURRENT FILING DATE: 2003-03-20
NUMBER OF SEQ ID NOS: 337


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; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528.237A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 133318
; TYPE: DNA
; ORGANISM: Drosophila
US-09-528-237A-20

Query Match      17.3%; Score 33.2; DB 22; Length 133318;
Best Local Similarity 61.6%; Pred. No. 66;
Matches 53; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY      26 CTGACAGCATATCTGTGCTGATTCGCTCATTTTCATATACCTTCGGGGAATAGATGT 85
      48226 CTCGACACGCAATATATATTCCTGTTTATTTCTGTAGACTTGGCTAAATGCTCA 48167
QY      86 GAAACCCCTATATAACGCGGCTTT 111
      48166 GAAAGCTCATAGATATATCGTTT 48141
DB

RESULT 15
US-09-948-128-318/C
; Sequence 318, Application US/09948128
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
; TITLE OF INVENTION: 17, METHODS OF DETECTION, AND USES THEREOF
; FILE REFERENCE: CL001294
; CURRENT APPLICATION NUMBER: US/09/948.128
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 465
; SEQ ID NO 318
; LENGTH: 12360069
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(12360069)
; OTHER INFORMATION: n - A,T,C or G
US-09-948-128-318

Query Match      17.1%; Score 32.8; DB 40; Length 12360069;
Best Local Similarity 61.9%; Pred. No. 3.6e+02;
Matches 52; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY      36 ATATCTTGTCGATTCGCTATTTTCATATACCTTCGGGGAATAGATGTGAACCCCTT 95
      7643639 AGATATTTCTTTTCACACCTACTGTATATCCCTCCGGTAATAGCATGACATATATA 7643580
QY      96 ATAAACGCGGCTTTTCGAGAAA 119
      7643579 ATGAAATACCTTTTCTGAGAAA 7643556
DB

Search completed: August 25, 2003, 21:54:32
Job time : 1571.9 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:46:38 ; Search time 30.8534 Seconds

(without alignments)
2746.715 Million cell updates/sec

Title: US-09-816-391A-1_COPY_1_192

Perfect score: 192

Sequence: 1 gcctggcgccggcgccatga.....tgaccacaagaagatgcttt 192

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCUTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	29.8	15.5	10303	4	US-09-634-238-410
C 2	29.2	15.2	3092	1	US-08-426-627-3
C 3	29.2	15.2	3126	2	US-08-477-396A-3
C 4	29.2	15.2	3253	1	US-08-426-627-5
C 5	29	15.1	1830121	4	US-09-557-884-1
C 6	29	15.1	1830121	4	US-09-643-990A-1
C 7	27.8	14.5	730	3	US-08-943-731-128
C 8	27.8	14.5	1257	1	US-08-330-154-1
C 9	27.8	14.5	1269	4	US-09-134-001C-2393
C 10	27.8	14.5	24183	3	US-08-943-731-3
C 11	27.6	14.4	336	4	US-09-328-352-692
C 12	27.4	14.3	7650	4	US-09-221-017B-911
C 13	27.4	14.3	202001	4	US-09-734-674-3
C 14	27.4	14.3	580073	4	US-08-545-528D-1
C 15	27.2	14.2	318	4	US-09-107-532A-3017
C 16	27.2	14.2	615	4	US-09-107-532A-2248
C 17	27.2	14.2	168575	4	US-09-426-290-1
C 18	27	14.1	1009	6	5223394-8
C 19	27	14.1	1244	2	US-08-204-288-3
C 20	27	14.1	3182	1	US-08-188-582-12
C 21	27	14.1	3182	1	US-08-646-715-12
C 22	27	14.1	3852	1	US-08-306-546C-1
C 23	27	14.1	3852	2	US-08-530-524A-1
C 24	27	14.1	4321	4	US-09-773-426A-4
C 25	27	14.1	13993	4	US-09-220-132-20
C 26	27	14.1	14070	4	US-09-108-006C-2
C 27	26.8	14.0	875	4	US-09-221-017B-671

C 28	26.8	14.0	1710	4	US-08-630-915A-189	Sequence 189, App
C 29	26.8	14.0	42571	4	US-09-810-347-3	Sequence 3, Appl
C 30	26.6	13.9	3484	4	US-09-308-090-1	Sequence 1, Appl
C 31	26.6	13.9	3484	4	US-09-380-090A-1	Sequence 1, Appl
C 32	26.6	13.9	129908	4	US-09-585-858-1	Sequence 1, Appl
C 33	26.4	13.7	927	4	US-09-328-352-2966	Sequence 2966, Ap
C 34	26.4	13.7	1230025	4	US-09-198-452A-1	Sequence 1, Appl
C 35	26.2	13.6	924	4	US-09-107-532A-620	Sequence 620, App
C 36	26.2	13.6	1610	3	US-09-347-803-19	Sequence 19, Appl
C 37	26.2	13.6	2005	4	US-08-936-165A-102	Sequence 102, App
C 38	26.2	13.6	2559	4	US-09-071-035-325	Sequence 325, App
C 39	26.2	13.6	2559	4	US-09-071-035-329	Sequence 329, App
C 40	26.2	13.6	2559	4	US-09-071-035-333	Sequence 333, App
C 41	26.2	13.6	2801	3	US-08-747-221B-30	Sequence 30, Appl
C 42	26.2	13.6	2801	3	US-08-747-221B-32	Sequence 32, Appl
C 43	26.2	13.6	2801	3	US-09-005-051-30	Sequence 30, Appl
C 44	26.2	13.6	2801	3	US-09-005-051-32	Sequence 32, Appl
C 45	26.2	13.6	2836	3	US-08-747-221B-24	Sequence 24, Appl

ALIGNMENTS

```

RESULT 1
US-09-634-238-410/c
; Sequence 410, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.104301
; CURRENT APPLICATION NUMBER: US/09/634,238
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410
; LENGTH: 10303
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-410

Query Match          15.5%; Score 29.8; DB 4; Length 10303;
Best Local Similarity 60.5%; Pred. No. 2;
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 112 CGCGAAGACATGCCCTGATCATGATGACACATGACCAAAAGCTTGCC 171
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 8088 CGAAGAAAGCGAAGCAAGCATGTTGGAAGATCATGACGCAAAAGATTGCGC 8029
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 172 CTGACCAAGAAAGATGCTTT 192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 8028 CGGCTCGAAAGATGCGGCTTT 8008
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
US-08-426-627-3
; Sequence 3, Application US/08426627
; Patent No. 5756664
; GENERAL INFORMATION:
; APPLICANT: Amann, Egon
; APPLICANT: Awawara-Hanamoto, Yoko
; APPLICANT: Kikuno, Reiko
; APPLICANT: Takeshita, Sunao

```

APPLICANT: Tezuka, Kenichi
TITLE OF INVENTION: No. 575664el Protein with Bone Formation
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,627
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,841
FILING DATE: 25-MAR-1993
APPLICATION NUMBER: JP 4-71501
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hammond, Alan W.
REGISTRATION NUMBER: 35,178
REFERENCE/DOCKET NUMBER: 02481-1285-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
FAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3092 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Placenta
FEATURE:
NAME/KEY: CDS
LOCATION: join(38..2375)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: join(101..2375)
US-08-426-627-3
Query Match 15.2%; Score 29.2; DB 1; Length 3092;
Best Local Similarity 59.8%; Pred. No. 2;
Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 89 AACCTTATAAAGCGGGTTTCGCAAGAACGCGCTAGTATCTTATGCAACATG 148
DB 626 AACCATTAATGCTTAATGGGCTTGCACCTTAATGCTGCAATTCATCGGAACAG 665
QY 149 GACTAGCAAAAGTCTGTCC 170
DB 686 ATTGCAACAAGTGTGTCTCC 707
RESULT 3
US-08-477-396A-3
Sequence 3, Application US/08477396A
Patent No. 5872335
GENERAL INFORMATION:
APPLICANT: Chen, Ian Bo
APPLICANT: Bao, Shideng
APPLICANT: Liu, Yuan
TITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF

TITLE OF INVENTION: ISOLATING SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnabln & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,396A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,488
FILING DATE: 29-OCT-1993
APPLICATION NUMBER: US 08/448,388
FILING DATE: 28-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12502
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCI-333BX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
FAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 43..2376
US-08-477-396A-3
Query Match 15.2%; Score 29.2; DB 2; Length 3126;
Best Local Similarity 59.8%; Pred. No. 2;
Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 89 AACCTTATAAAGCGGGTTTCGCAAGAACGCGCTAGTATCTTATGCAACATG 148
DB 649 AACCATTAATGCTTAATGGGCTTGCACCTTAATGCTGCAATTCATCGGAACAG 708
QY 149 GACTAGCAAAAGTCTGTCC 170
DB 709 ATTGCAACAAGTGTGTCTCC 730
RESULT 4
US-08-426-627-5
Sequence 5, Application US/08426627
Patent No. 575664
GENERAL INFORMATION:
APPLICANT: Amann, Egon
APPLICANT: Otawara-Hamamoto, Yoko
APPLICANT: Kikuno, Reiko
APPLICANT: Takeshita, Sunao
APPLICANT: Tezuka, Kenichi
TITLE OF INVENTION: No. 575664el Protein with Bone Formation
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,627
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,841
FILING DATE: 25-MAR-1993
APPLICATION NUMBER: JP 4-71501
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hammond, Alan W.
REGISTRATION NUMBER: 35,178
REFERENCE/DOCKET NUMBER: 02481-1285-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3253 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: osteosarcoma
FEATURE:
NAME/KEY: CDS
LOCATION: join(32..2540)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: join(97..2540)
US-08-426-627-5

Query Match 15.2%; Score 29.2; DB 1; Length 3253;
Best Local Similarity 59.8%; Pred. No. 2.1;
Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

DB 89 ACCCTATATAAGCGGGTTTGGCAGAAACATGCCGTATCATGTATGACAACTG 148
|||||
DB 620 AACCATATTCCTTAATGCGGTGTCATGCTTAATGCTCGAATCATCAGGAAACAC 679
|||||
DB 149 GACTAACCAAAAGTCTGTCC 170
|||||
DB 680 ATTGCACAACAATGCTGTGCC 701
|||||

RESULT 5
US-09-557-884-1/c
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fieischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue

CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: P8186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 15.1%; Score 29; DB 4; Length 1830121;
Best Local Similarity 53.0%; Pred. No. 28;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

DB 31 CAACATATATCTGTGCTGATTCGCTATTTTCATACCTTCGGGAAATAGATGAAAA 90
|||||
DB 1014886 CACCAATATTAATTCGATGATGTTTATTTGAAATTAATTAATGATGAAAAATTAATCTTGC 1014827
|||||
DB 91 CCCTATATAAGCGGGTTTGGCAGAAACATGCCGTATCATGTATGACAACTG 147
|||||
DB 1014826 GCCATATACAAACATGTTTTCATGAGCGTGATTAAGATTTCGATCCCAACAT 1014770
|||||

RESULT 6
US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fieischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A

FILED DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match 15.1%; Score 29; DB 4; Length 1830121;
Best Local Similarity 53.0%; Pred. No. 28;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 31 CAAGCATATCTGTCTGATGCTATTTTCAATACCTTCGGGGAATGATGTGAAA 90
DB 1014886 CACCAAAATTAATTTGGATGGTTTATTTTGAATAAATATGTAATAAATATCTTGC 1014827
QY 91 CCCTTATTAACCGCGCTTTCAGAGAAACATGCCGATGATCATGATGACAACAT 147
DB 1014826 GCCATATACAGATGTTTTCATGAGCGTGATGATGATCTGATCTCAACAT 1014770

RESULT 7
US-08-943-731-128/C
Sequence 128, Application US/08943731
Patent No. 6265157
GENERAL INFORMATION:
APPLICANT: PROCKOP, DARWIN J.
APPLICANT: SPOTILA, LORETTA D.
APPLICANT: DELTAS, CONSTANTINOS D.
APPLICANT: SEREDA, LARISA
APPLICANT: LARSON, ANDREA W.
APPLICANT: PACK, MICHAEL
APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORRKO, JARMO
TITLE OF INVENTION: ALA-KORRKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
NUMBER OF SEQUENCES: 666
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADDEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322

FILED DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9398-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-943-731-128

Query Match 14.5%; Score 27.8; DB 3; Length 730;
Best Local Similarity 65.1%; Pred. No. 3.5;
Matches 41; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 130 TATCATGATGACATGAGCTAAGCAAAAGTCCTTGCCCTGACCAAGAGATGC 189
DB 374 TTTCAGAGTACAGACCTTGACCAAGCTCAGCTATCCCTGCGCTGAAAGCTGC 315
QY 190 TTT 192
DB 314 TCT 312

RESULT 8
US-08-330-154-1
Sequence 1, Application US/08330154
Patent No. 5587307
GENERAL INFORMATION:
APPLICANT: Alborn Jr., William E
APPLICANT: Hoskins, Joann L
APPLICANT: Skatrud, Paul L
TITLE OF INVENTION: Unal, Serhat
TITLE OF INVENTION: FEM A GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
TITLE OF INVENTION: THE FEM A GENE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Division/AEH
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,154
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/208,925
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US/08/057,163
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hamilton, Amy E
REGISTRATION NUMBER: 33,894
REFERENCE/DOCKET NUMBER: X-8894
TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-276-3169
TELEFAX: 317-276-1294
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1257
US-08-330-154-1

Query Match 14.5%; Score 27.8; DB 1; Length 1257;
Best Local Similarity 62.0%; Pred. No. 4.4;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY 89 AACCCCTATTAAGACGCGGTTTCGAGAAACATGCGCTATGATCATGATGACATG 148
DB 694 AAACATTAATAAGACCGGTGTTTAGTACCACTAGCCTATATTACTTGTGATGATATA 753
OY 149 GACTAAGCAA 159
DB 754 GAGGAACATAA 764

RESULT 9
US-09-134-001C-2393
Sequence 2393, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stramm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2393
LENGTH: 1269
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2393

Query Match 14.5%; Score 27.8; DB 4; Length 1269;
Best Local Similarity 62.0%; Pred. No. 4.4;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
OY 89 AACCCCTATTAAGACGCGGTTTCGAGAAACATGCGCTATGATCATGATGACATG 148
DB 703 AAACATTAATAAGACCGGTGTTTAGTACCACTAGCCTATATTACTTGTGATGATATA 762
OY 149 GACTAAGCAA 159
DB 763 GAGGAACATAA 773

RESULT 10
US-08-943-731-3/c
Sequence 3, Application US/08943731
Patent No. 6265157
GENERAL INFORMATION:
APPLICANT: PROCKOP, DARWIN J.
APPLICANT: SPOTILA, LORETTA D.
APPLICANT: DETTAS, CONSTANTINOS D.
APPLICANT: SEREDA, LARISA
APPLICANT: LARSON, ANDREA W.
APPLICANT: PACK, MICHAEL

APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORKKO, JARMO
APPLICANT: ALA-KORKKO, LEENA, et al
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24183 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-943-731-3

Query Match 14.5%; Score 27.8; DB 3; Length 24183;
Best Local Similarity 65.1%; Pred. No. 14;
Matches 41; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
OY 130 TATCATTTGATGACACATGAGCTAGCAAAAGTGTTCCTCCCTACCCAGAAAGATGC 189
DB 10606 TTTCGAAGTGCACACCTTGCACCAAGCTGACTAGCTACCCCTGCGAAGGCTGC 10547
OY 190 TTT 192
DB 10546 TCT 10544

RESULT 11
US-09-328-352-692/c
Sequence 692, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 692

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1
LENGTH: 580073
TYPE: DNA
ORGANISM: Mycoplasma genitalium
US-08-545-528D-1

Query Match 14.3%; Score 27.4; DB 4; Length 580073;
Best Local Similarity 59.7%; Pred. No. 66;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 91 CCCATTAAGCGCGGTTTGCAGAAACATGCGCTAGTATCATGTAGTACAAATGGA 150
114603 CCCATCAGAGAGATGCTTTCAGTACATGATGATGTTGTGATCTTGTCTAACAAAGAAA 114662

DB 151 CTACGCAAAAGTGTG 167
114663 TGAAAAAACATGCTTG 114679

RESULT 15

US-09-107-532A-3017
Sequence 3017, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-8277
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3017:

SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:

NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...318
SEQUENCE DESCRIPTION: SEQ ID NO: 3017:
US-09-107-532A-3017

Query Match

14.2%; Score 27.2; DB 4; Length 318;

Best Local Similarity 61.1%; Pred. No. 4.1;
Matches 44; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 112 CCAGAAACATGCGCTAGTATCATGTAGTACAAATGAGCTAGCAAAAGTGTGCTCC 171

DB 96 CGAGAAAAATGTGCGTGTGTCTGATTCGAAACATGACATAGACAAATGCGCTTATC 155

QY 172 CTGACCCAGAA 183

DB 156 CTACCAATGAA 167

Search completed: August 25, 2003, 19:52:21
Job time : 38.8534 secs

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OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:46:38 ; Search time 96.4169 Seconds

(without alignments)
2746.715 Million cell updates/sec

Title: US-09-816-391A-1

Perfect score: 600

Sequence: 1 gctggcgcgcgcgcatga.....tattcgactagtcgacg 600

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCUS.COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67.2	11.2	363	US-09-252-991A-7263	Sequence 7263, Ap
2	65.6	10.9	426	US-09-252-991A-13810	Sequence 13810, A
3	64.2	10.7	312	US-09-252-991A-13634	Sequence 13634, A
4	63.4	10.6	312	US-09-252-991A-13917	Sequence 13917, A
5	46.8	7.8	477	US-09-252-991A-3732	Sequence 3732, Ap
6	46.8	7.8	567	US-09-252-991A-3828	Sequence 3828, Ap
7	43.6	7.3	16075	US-09-096-942-1	Sequence 1, Appl1
8	43.6	7.3	16075	US-09-096-867-1	Sequence 1, Appl1
9	42	7.0	306	US-09-252-991A-14703	Sequence 14703, A
10	42	7.0	498	US-09-252-991A-15197	Sequence 15197, A
11	40.6	6.8	732	US-09-252-991A-8860	Sequence 8860, Ap
12	40.6	6.8	1047	US-09-252-991A-9034	Sequence 9034, Ap
13	40.6	6.8	1464	US-09-252-991A-8971	Sequence 8971, Ap
14	40.6	6.8	1494	US-09-252-991A-9117	Sequence 9117, Ap
15	39.6	6.6	2178	US-09-252-991A-7630	Sequence 7630, Ap
16	39.6	6.6	3030	US-09-252-991A-7921	Sequence 7921, Ap
17	39.6	6.6	4403765	US-09-103-840A-2	Sequence 2, Appl1
18	39.6	6.6	4411529	US-09-103-840A-1	Sequence 1, Appl1
19	38.4	6.4	765	US-09-252-991A-4768	Sequence 4768, Ap
20	38.4	6.4	1047	US-09-252-991A-4739	Sequence 4739, Ap
21	37.8	6.3	309	US-09-252-991A-12150	Sequence 12150, A
22	37.6	6.3	858	US-09-095-855-200	Sequence 200, App
23	37.6	6.3	858	US-09-205-426-200	Sequence 200, App
24	37.4	6.2	555	US-09-252-991A-11170	Sequence 11170, A
25	37.4	6.2	969	US-09-199-637A-48	Sequence 48, Appl
26	37.4	6.2	1017	US-09-199-637A-46	Sequence 46, Appl
27	37.4	6.2	1083	US-09-252-991A-11841	Sequence 11841, A

28	37.4	6.2	1407	US-09-252-991A-11543	Sequence 11543, A
29	37.4	6.2	1608	US-09-252-991A-11665	Sequence 11665, A
30	37.4	6.2	2025	US-09-199-637A-50	Sequence 50, Appl
31	37.4	6.2	2304	US-09-252-991A-11691	Sequence 11691, A
32	37.4	6.2	42235	US-09-199-637A-1	Sequence 1, Appl1
33	37.2	6.2	1428	US-09-252-991A-2357	Sequence 2357, Ap
34	37.2	6.2	1449	US-09-252-991A-2559	Sequence 2559, Ap
35	37.2	6.2	2343	US-09-252-991A-2275	Sequence 2275, Ap
36	37	6.2	2943	US-08-042-747A-7	Sequence 7, Appl1
37	36.6	6.1	77536	US-09-410-551B-1	Sequence 1, Appl1
38	36.6	6.1	4403765	US-09-103-840A-2	Sequence 2, Appl1
39	36.6	6.1	4411529	US-09-103-840A-1	Sequence 1, Appl1
40	36.2	6.0	375	US-09-199-637A-52	Sequence 52, Appl
41	35.4	5.9	666	US-09-252-991A-10065	Sequence 10065, A
42	35.4	5.9	711	US-09-252-991A-12233	Sequence 12233, A
43	35.4	5.9	876	US-09-252-991A-9769	Sequence 9769, Ap
44	35.4	5.9	1095	US-09-252-991A-12376	Sequence 12376, Ap
45	35.4	5.9	1188	US-09-252-991A-12167	Sequence 12167, A

ALIGNMENTS

```

RESULT 1
US-09-252-991A-7263
Sequence 7263, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7263
LENGTH: 363
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7263

Query Match
Best Local Similarity 53.4%; Pred. No. 5.9e-11;
Matches 141; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 205 AAGTCTGACCTGTTTCGAAGATGCGCCGAGAAAGTTCACACCTGACGAGCTCAGGCGGAG 264
DB AAACGAGAACTAAGCCGCGCTATGCGGAAAGCGGATCTCACCAAGAACAGGACCAAT 156
QY 265 GCTGCTGTTAAGCCCTTCAGAGATGTTCTCGAGGCTAGAGTGCAGAGTGCAGAGCGCTG 324
DB CGCGTCTCAACGCCGCTGTTGATGAATACCCGCGCGCTGAACCCGAGAACGAGAGGCTG 216
QY 325 AAGTCAACCGGCGTTCCTCGCTGAGCGGCTCAAGCGCCGCTGCACCGCGGAGC 384
DB ACCCTGCTGCTTTCGCGACCTTCCTCCACAGCCATCGGAGCGGAGCCGACAGAGAAAG 276
QY 385 CCGGCACTGGCGAGCATTTGACATTCGCGCTTCACGCGCTTCATCTCCGCTGCG 444
DB CCGGAGACCGGCGGCGGCTGATGAATTAAGCCAGCAACCGTCCGCTTCAAGCCGCGG 336
QY 445 TCCCTGCTGAAGAAAGCGCTCACC 468
DB AAGCCCTCGCGCGAGCGGCTCAAC 360

RESULT 2
US-09-252-991A-13810/c
Sequence 13810, Application US/09252991A

```



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; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3732
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3732

```

Query Match 7.8%; Score 46.8; DB 4; Length 477;
Best Local Similarity 47.9%; Pred. No. 0.00011;

Matches 135; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

```

QY 193 ATGGCATACAAAGTCTGACCTGTTTCCGAGATCGCCGAGAAATCCACCTGACCAAG 252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 196 ATGGCACTGACCAAGACCACTGATCCAGACATGCGCAACCATCGACGCGCAAG 255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 253 GCTCAGCGCGAGGCTCTGTAAAGCCTTCAGATGTGTTCGTGAGGCTATGAATCC 312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 256 ACCACCGTTCGAGCGCGCTCGACAGCTCGCCGAGATGCTCAAGAGACGCCCTGAGAAC 315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 313 GCGCAAGGCGCTGAGCTACCGGCGCTGTCTCCGCTGACCGCGCTCAAGCGCGGCTCG 372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 316 GATGGCGAATACCTGCGCGGCTATCGCAAGCTGAAAGTCTCCGAGGCTCCCGCGCG 375
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 373 ACCGCGCGCAACCGCGGCGCTGCGGCGAGCAGATTGACATTCGCGCTCTTACGCGCTTGT 432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 376 ACCGCGCGCAACCGCGGCGAGCGCAAGGAGATGAGATGCTGCCAAGGCTGTAGCCAAAG 435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 433 ATCTCGCTGGCTCTCTGTGAAGAAAGCGCTACCGAGTGA 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 436 TTCTGTCGCGCAAGGCACTGACCGAGATCAACGCGCTGA 477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 6

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US-09-252-991A-3828/C
; Sequence 3828, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3828
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3828

```

Query Match 7.8%; Score 46.8; DB 4; Length 567;
Best Local Similarity 47.9%; Pred. No. 0.00011;

Matches 135; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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QY 193 ATGGCATACAAAGTCTGACCTGTTTCCGAGATCGCCGAGAAATCCACCTGACCAAG 252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 557 ATGGCACTGACCAAGACCACTGATCCAGACATGCGCAACCATCGACGCGCAAG 498
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 253 GCTCAGCGCGAGGCTCTGTAAAGCCTTCAGATGTGTTCGTGAGGCTATGAATCC 312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 497 ACCACCGTTCGAGCGCGCTCGACAGCTCGCCGAGATGCTCAAGAGACGCCCTGAGAAC 438
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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```

QY 313 GCGCAAGGCGCTGAGCTACCGGCGCTGTCTCCGCTGACCGCGTCAAGCGCGGCTCG 372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 437 GATGGCGAATACCTGCGCGGCTATCGCAAGCTGAAAGTCTCCGAGGCTCCCGCGCG 378
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 373 ACCGCGCGCAACCGCGGCGCTGCGGCGAGCAGATTGACATTCGCGCTTCTTACGCGCTTGT 432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 377 ACCGCGCGCAACCGCGGCGAGACCGCGCAAGCGGATGAGATCTCTTCCCAAGCGTGTAGCCAAAG 318
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 433 ATCTCGCTGGCTCTCTGTGAAGAAAGCGCTACCGAGTGA 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 317 TTCTGTCGCGCAAGGCACTGACCGAGATCAACGCGCTGA 276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 7

```

US-09-096-942-1
; Sequence 1, Application US/09096942
; Patent No. 6027925
; GENERAL INFORMATION:
; APPLICANT: Pollock, Thomas J
; APPLICANT: Mikolajczak, Marcia
; APPLICANT: Yamazaki, Motohide
; APPLICANT: Thorne, Linda
; APPLICANT: Armentrout, Richard W
; TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
; FILE REFERENCE: seq list for appl filed from pro. appl
; CURRENT APPLICATION NUMBER: US/09/096,942
; EARLIER APPLICATION NUMBER: 60/049,428
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 16075
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
; PUBLICATION INFORMATION:
US-09-096-942-1

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Query Match

7.3%; Score 43.6; DB 3; Length 16075;
Best Local Similarity 47.7%; Pred. No. 0.0047;

Matches 127; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

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QY 193 ATGGCATACAAAGTCTGACCTGTTTCCGAGATCGCCGAGAAATCCACCTGACCAAG 252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 33 ATGGATGAGAAAGCGAGATGCGGAGCGCTGTGTCGAGAGTGGCGCTGAAACAG 92
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 253 GCTCAGCGCGAGGCTCTGTAAAGCCTTCAGATGTGTTCGTGAGGCTATGAATCC 312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 93 CGTAGGCGGAGGAATTCGTGACGCGCTTTTCATGTGCTGCGCGAGTGCACACTGGAGCAG 152
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 313 GCGCAAGGCGTGAAGCTACCGGCGCTGTCTCCGCTGAGCGCGTCAAGCGCGGCTCG 372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 153 GCGCGTAGGTTGAAGTGTGCGGCTTTCGCAACTTCATCTGCGCGCAAGAACCAACG 212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 373 ACCGCGCGCAACCGCGGCGCTGCGGCGAGATTCAGATTCGCGGCTTCTTACGCGCTTGT 432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 213 CCGCGTGCATTCACCAAGACCGGTGAGGAATTCGATCTGCGCAGAGCGGTGTACC 272
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 433 ATCTCGCTGGCTCTCTGTGAAGAAAGCGCTACCGAGTGA 458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 273 TTCTGTCGCGCGCGCAAGAACTCAAGGA 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 8

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US-09-096-867-1
; Sequence 1, Application US/09096867
; Patent No. 6030817
; GENERAL INFORMATION:
; APPLICANT: Pollock, Thomas J
; APPLICANT: Mikolajczak, Marcia
; APPLICANT: Yamazaki, Motohide
; APPLICANT: Thorne, Linda

```



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FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7630
; LENGTH: 2178
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7630

Query Match      6.68; Score 39.6; DB 4; Length 2178;
Best Local Similarity 60.0%; Pred. No. 0.032;
Matches 66; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

OY 272 TTAACGCTTCAGAGATGTGTCGAGGCTATGAAGTCCGGCGAAGGCTGAAGCTCA 331
    ||||| ||||| || ||||| || ||||| ||||| ||||| ||||| |||||
DB 1880 TCAACGATTTACACAGCCCTTGCAGCCGCCGCCCTGTACGACAGCAATGGCTGATGCTGG 1821
    ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
OY 332 CCGGCTGTCTCCGCTGAGCGCGCTCAAGCGCCCGGCTCGACCGCGCGC 381
    ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
DB 1820 CCGACCTGCAACGCGGCGGACACCTCAAGCTGCCGCGCCGCGCTGACCGC 1771
    ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Search completed: August 25, 2003, 19:52:13
Job time : 106.417 secs
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Result	Query	Match	Length	ID	Description
No.	Score				
1	500	100.0	600	9	Sequence 1, App11
2	77.6	12.9	279	14	Sequence 5111, A
3	77.6	12.9	9023608	14	Sequence 1, App
4	68.8	11.5	273	14	Sequence 71, App
5	64.2	10.7	273	9	Sequence 7753, App
6	61.8	10.3	651	14	Sequence 2611, A
7	61.8	10.3	9025608	14	Sequence 1, App
8	48.2	8.0	273	9	Sequence 9847, App
9	41.8	7.0	273	9	Sequence 5974, App
10	39	6.5	1326	14	Sequence 12, App
11	39	6.5	3411	14	Sequence 9872, A
12	38.4	6.4	14	US-10-198-846-9872	Sequence 7900, App
13	37.6	6.4	696	9	Sequence 26, App
14	37.6	6.3	858	12	Sequence 200, App
15	37.6	6.3	1089	13	Sequence 6834, A
16	37.4	6.2	4447	9	Sequence 27737, A
				US-09-864-761-27737	

17	37.4	6.2	969	11	US-09-975-719-48	Sequence 48, App
18	37.4	6.2	2025	11	US-09-975-719-46	Sequence 46, App
19	37.4	6.2	1017	11	US-09-975-719-50	Sequence 50, App
20	37.4	6.2	1290	11	US-09-999-121-7	Sequence 7, App
21	37.4	6.2	25760	11	US-09-999-121-13	Sequence 13, App
22	37.4	6.2	43233	11	US-09-975-719-1	Sequence 1, App
23	37.2	6.2	13935	9	US-09-815-242-8008	Sequence 8008, App
24	37	6.2	1830-	14	US-10-081-872-181	Sequence 181, App
25	37	6.2	6223	13	US-10-108-605-320	Sequence 320, App
26	36.8	6.1	457	9	US-09-815-242-3785	Sequence 3785, App
27	36.6	6.1	385	9	US-09-864-761-11106	Sequence 11106, A
28	36.6	6.1	1317	14	US-10-156-761-4093	Sequence 4093, App
29	36.6	6.1	1425	14	US-10-156-761-3337	Sequence 3337, App
30	36.6	6.1	1830	14	US-10-081-872-181	Sequence 181, App
31	36.2	6.0	276	9	US-09-815-242-9221	Sequence 9221, App
32	36.2	6.0	375	11	US-09-975-719-52	Sequence 52, App
33	36	6.0	1002	14	US-10-156-761-2166	Sequence 2166, App
34	36	6.0	1299	14	US-10-156-761-2376	Sequence 2376, App
35	35.6	5.9	765	14	US-10-156-761-7195	Sequence 7195, App
36	35.4	5.9	1491	14	US-10-156-761-1868	Sequence 1868, App
37	35.2	5.9	669	14	US-10-156-761-213	Sequence 213, App
38	35.2	5.9	996	9	US-09-815-242-7775	Sequence 7775, App
39	35.2	5.9	1020	14	US-10-156-761-3960	Sequence 3960, App
40	35.2	5.9	4512	14	US-10-156-761-2222	Sequence 2222, App
41	35	5.8	1428	14	US-10-156-761-3841	Sequence 3841, App
42	34.8	5.8	876	14	US-10-156-761-7128	Sequence 7128, App
43	34.8	5.8	1086	14	US-10-156-761-3194	Sequence 3194, App
44	34.8	5.8	1281	14	US-10-156-761-3352	Sequence 3352, App
45	34.6	5.8	396	14	US-10-156-761-2292	Sequence 2292, App

ALIGNMENTS

RESULT 1
 US-09-816-391A-1
 ; Sequence 1, Application US/09816391A
 ; Patent No. US20020054865A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FUJIMORI, MINDOTU
 ; APPLICANT: TANIGUCHI, Shunichiro
 ; APPLICANT: AMANO, Jun
 ; APPLICANT: YAZAWA, Kazuyuki
 ; APPLICANT: KANO, Yasunobu
 ; APPLICANT: NAKAMURA, Toshiyuki
 ; APPLICANT: SASAKI, Takayuki
 ; TITLE OF INVENTION: Anaerobic bacterium as a drug for cancer gene therapy
 ; FILE REFERENCE: 2001-WMC/01736
 ; CURRENT APPLICATION NUMBER: US/09/816,391A
 ; CURRENT FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP 00/287688
 ; PRIOR FILING DATE: 2000-09-21
 ; NUMBER OF SEQ ID NOS: 3
 ; SEQ ID NO 1
 ; LENGTH: 600

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; ORGANISM: Bifidobacterium longum
;
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: (193)..(471)
US-09-816-391A-1

Query Match          100.0%   Score 600; DB 9; Length 600;
Best Local Similarity 100.0%   Pred. No. 76-194;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SGTGGGGGGGGGGCATGAAGTCGCTTGACACAAATCTTGTCGATGCTATTT 60
Db 1 GCTGGGGGGGGGGCCGACGAGAGTGGCTTGACAAACCAATCTTGTCGATGCTATTT 60
QY 61 TCAAACTCTGGGGGAAATAGATGTGAAACCTTTATTAACGGGGTTTTGCGACAAAC 120
Db 61 TCAAACTCTGGGGGAAATAGATGTGAAACCTTTATTAACGGGGTTTTGCGACAAAC 120

OY	121	ATGCGCTAGTATCATTTGATGAGACATATGAGCTAAAGCAAAATCGTTCTCCCTGACCCAA	180
	122	ATGCGCTAGTATCATTTGATGAGACATATGAGCTAAAGCAAAATCGTTCTCCCTGACCCAA	180
Db	121	ATGCGCTAGTATCATTTGATGAGACATATGAGCTAAAGCAAAATCGTTCTCCCTGACCCAA	180
OY	181	GAAGATGCTTTATGCGATACACAAGTCTGACCTCGTTTCGAAAGATGCCAGAAAGTCC	240
	182	GAAGATGCTTTATGCGATACACAAGTCTGACCTCGTTTCGAAAGATGCCAGAAAGTCC	240
Db	181	GAAGATGCTTTATGCGATACACAAGTCTGACCTCGTTTCGAAAGATGCCAGAAAGTCC	240
OY	241	AACCTGACCAAGGCTCAGGCGGAGGCTCTGTAAAGCGCTTCAGAGATGTTGTTGCTGAG	300
	242	AACCTGACCAAGGCTCAGGCGGAGGCTCTGTAAAGCGCTTCAGAGATGTTGTTGCTGAG	300
Db	241	AACCTGACCAAGGCTCAGGCGGAGGCTCTGTAAAGCGCTTCAGAGATGTTGTTGCTGAG	300
OY	301	GGTATGAATCCGGGCGAGGCGCTGGAAGCTCAACGGGCTGTCTTCGCTGAGCGGCTCAAG	360
	302	GGTATGAATCCGGGCGAGGCGCTGGAAGCTCAACGGGCTGTCTTCGCTGAGCGGCTCAAG	360
Db	301	GGTATGAATCCGGGCGAGGCGCTGGAAGCTCAACGGGCTGTCTTCGCTGAGCGGCTCAAG	360
OY	361	CGCGCGGCTCGCACCGGCGCCAAACCCGGGCACTGGCGGAGCAGATTGACATTCCGGCTTCC	420
	362	CGCGCGGCTCGCACCGGCGCCAAACCCGGGCACTGGCGGAGCAGATTGACATTCCGGCTTCC	420
Db	361	CGCGCGGCTCGCACCGGCGCCAAACCCGGGCACTGGCGGAGCAGATTGACATTCCGGCTTCC	420
OY	421	TACGGGCTTCTGATCTCGCTGGCTCCCTCGTGAAGAAGGCGCTCACCGAGTAGCTTCT	480
	422	TACGGGCTTCTGATCTCGCTGGCTCCCTCGTGAAGAAGGCGCTCACCGAGTAGCTTCT	480
Db	421	TACGGGCTTCTGATCTCGCTGGCTCCCTCGTGAAGAAGGCGCTCACCGAGTAGCTTCT	480
OY	481	GCTCGTAGCGATTACTTGACGATTACTGACGACAAAGACCCCGACCGAGATGGTCCGGG	540
	482	GCTCGTAGCGATTACTTGACGATTACTGACGACAAAGACCCCGACCGAGATGGTCCGGG	540
Db	481	GCTCGTAGCGATTACTTGACGATTACTGACGACAAAGACCCCGACCGAGATGGTCCGGG	540
OY	541	TCTTTTGTGTTGGGCGCTGACGCGTTGTCCAAACCGATTATTCGGGACTAGTTCAAGC	600
	542	TCTTTTGTGTTGGGCGCTGACGCGTTGTCCAAACCGATTATTCGGGACTAGTTCAAGC	600
Db	541	TCTTTTGTGTTGGGCGCTGACGCGTTGTCCAAACCGATTATTCGGGACTAGTTCAAGC	600

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1      RESULT 2
2      US-10-156-761-5111
3      ; Sequence 5111, Application US/10156761
4      ; Publication No. US20030119018A1
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: OMURA, SATOSHI
9      ; APPLICANT: IKEDA, HARUO
10     ; APPLICANT: ISHIKAWA, JUN
11     ; APPLICANT: HORIKAWA, HIROSHI
12     ; APPLICANT: SHIBA, TADAYOSHI
13     ; APPLICANT: SAKAKI, YOSHIYUKI
14     ; APPLICANT: HATTORI, MASAHIRA
15     ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
16     ; FILE REFERENCE: 249-262
17     ;
18     ; CURRENT APPLICATION NUMBER: US/10/156,761
19     ;
20     ; CURRENT FILING DATE: 2002-05-29
21     ;
22     ; PRIOR APPLICATION NUMBER: JP 2001-204089
23     ;
24     ; PRIOR FILING DATE: 2001-05-30
25     ;
26     ; PRIOR APPLICATION NUMBER: JP 2001-272697
27     ;
28     ; PRIOR FILING DATE: 2001-08-02
29     ;
30     ; NUMBER OF SEQ ID NOS: 15109
31     ;
32     ; SEQ ID NO 5111
33     ;
34     ; LENGTH: 279
35     ;
36     ; TYPE: DNA
37     ;
38     ; ORGANISM: Streptomyces avermitilis
39     ;
40     ; FEATURE:
41     ;
42     ; NAME/KEY: CDS
43     ;
44     ; LOCATION: (1)..(279)
45     ;
46     ; US-10-156-761-5111

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	Best Match	Similarity	Score	DB	Length
Qy	210	76.9%	7.6	279	269
Db	12	58.8%	7.6	279	269
Matches	153	Conservative	0	Mismatches	104
				Indels	3
				Gaps	1
Yy	270	76.9%	7.6	279	269

Db 72 TCTGGCCGCTTTCGCCGAGACCGTCGGCCGAGATCGTTGGCCAAAGGCGCAGCAAGAGTCAC 131

QY 327 GCTACACCGGCGCTTCTTCGCGCTGAGCGCGTCAAGCGCCCGCTCGCACCGCGCGCAACC 386

Db 132 CATCCCGCGGCTTCTGACCTTCGAGCGCCACCCACCGCTGCGCACCGCGCGTAACC 191

QY 387 GCGCAGTGGCGAGAGATTGACATTCGCGGCTTCCTACGCGGTTCTGATCTCGCTGGCTC 446

Db 192 GCAGACCGGGGACCCGATTCAGATCCCGGCGGGGTACAGCGTCAAGGTTCTCCGGGGCTC 251

QY 447 CCTGCTGAGAGGCGCTCA 466

Db 252 GAAGCTCAAGAAAGCCGCCA 271

```

RESULT 3
US-10-156-761-1
: Sequence 1, Application US/10156761
: Publication No. US20030119018A1
: GENERAL INFORMATION:
: APPLICANT: OMURA, SATOSHI
: APPLICANT: IKEDA, HARUO
: APPLICANT: ISHIKAWA, JUN
: APPLICANT: HORIKAWA, HIROSHI
: APPLICANT: SHIBA, TADAYOSHI
: APPLICANT: SAKAKI, YOSHIYUKI
: APPLICANT: HATTORI, MASAHIRA
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-262
: CURRENT APPLICATION NUMBER: US/10/156,761
: CURRENT FILING DATE: 2002-05-29
: PRIOR APPLICATION NUMBER: JP 2001-204089
: PRIOR FILING DATE: 2001-05-30
: PRIOR APPLICATION NUMBER: JP 2001-272697
: PRIOR FILING DATE: 2001-08-02
: NUMBER OF SEQ ID NOS: 15109
: SEQ ID NO 1
: LENGTH: 9025608
: TYPE: DNA
: ORGANISM: Streptomyces avermitilis
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: (4187715)
: OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

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	Query Match	Best Local Similarity	12.9%	Score 77.6	DB 14	Length 9025608	
	Matches	153	Conservative	0	Mismatches 104	Indels 3	Gaps 1
Oy	210	TGACCTGTTTCGAAGATCGCCCGAAGATCCACCTGATACCCAGGCTAGAGCCGAGGCTGC					
Db	6227520	TGACCTGTTGTCGCCGCTGCGCCGACCCGCGGAGATACCCGCAAGAGAGCCGCGCT					
Oy	270	TGTTAAGCCCTTCAGGATGTTGTCGTCGAG---GCTATGAAGTCCGCGGAGAGGCTGAA					
Db	6227580	TCTGGCCGCGTGTCCCGAGACCGTGGCGAGATGTTGCCAAGGGCCAGAGAAAGTCAAC					
Oy	327	GCATCAGCGGCTGTTCTCCGCTGAGCGCCGTCACGCCCGGCTGCAACCGGCCCAACC					
Db	6227640	CATCCCGCGGCTCTTGACCTTCGAGGCGACACCAACCGTGCCTGCAACCGCGCTAACCC					
Oy	387	GCGCATGCGCGAGAGATTGACATTCGCGGCTCTCTACGGGCTTCTGTAATCTCCGCTGGCTC					
Db	6227700	GCAACCGGCGGACCGAATCCAGATCCCGGGGGGCTACAGCGTCAAGGTCTCCGGGGGCTC					
Oy	447	CCTGCTGAAGAGGCGCTCA					
Db	6227760	GAAAGTCAAGAAAGCCGCA					

RESULT 4

US-10-127-032-71
; Sequence 71, Application US/10127032
; Publication No. US20030113742A1
; GENERAL INFORMATION:
; APPLICANT: Whiteley, Marvin
; APPLICANT: Bangera, M. Gita
; APPLICANT: Lory, Stephen
; APPLICANT: Greenberg, Everett Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
; FILE OF INVENTION: BIOFILM FORMATION
; FILE REFERENCE: 012-070CP
; CURRENT APPLICATION NUMBER: US/10/127,032
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/285,190
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/344,142
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-127-032-71

Query Match 11.5%; Score 68.8; DB 14; Length 273;
Best Local Similarity 53.8%; Pred. No. 6, 2e-13;
Matches 142; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

OY 205 AAGTGTGACCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCGGAG 264
DB 7 AACACGAACTAGCGCCGCTATCGCCGAAAGGCGGATCTACCAAGAACAGGCGCAAT 66
OY 265 GCTGTGTAAACCGCTTCCAGATGTGTCTGCGAGGCTATGAAGTCCGCGCAAGGCGCTG 324
DB 67 CGCGTTCACGCGCCCTGTTGATGAAATCACCGGCGCTGACACCGCAAGGACAGCGTG 126
OY 325 AAGCTACCGGCTTCTCCGCTGAGCGGCTGACAGCGCGGCTGCGACGCGGCGGCGCAAC 384
DB 127 ACCGTGCGGTTCGCGACCTTCTGCAAGCCCATCGGAGCGCGGCGGGAAGAAC 186
OY 385 CCGGCGACTGGCGAGCAATTCACATTCGCGCTTCTTACGCGGCTTCTGATCTCCGCTGCG 444
DB 187 CCGGAGACCGGCGGCGGCGGCTGAAATCAAGGCGGCAACACAGCTGCGCTTCAAGCGGCG 246
OY 445 TCCGCTGCGAAGAGCGCGCTCAC 468
DB 247 AAGCGCTGCGGCGGCGGCTCAAC 270

RESULT 5

US-09-815-242-7753
; Sequence 7753, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7753
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(273)
US-09-815-242-7753

Query Match 10.7%; Score 64.2; DB 9; Length 273;
Best Local Similarity 52.4%; Pred. No. 2, 3e-11;
Matches 141; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

OY 202 AACAGTGTGACCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCG 261
DB 4 AACAGTGTGACCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCG 63
OY 262 GAGGCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCG 321
DB 64 GCTGCGGCTGAGGCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCG 123
OY 322 CTGAAGTGTGACCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCG 381
DB 124 GTGCTGCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCG 183
OY 382 AACCGGCGGCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCG 441
DB 184 AACCGGCGGCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCG 243
OY 442 GGCTGCTGCTTTCGAAATCGCCAGAAATCCACCTGACCAAGGCTGAGGCG 470
DB 244 GGTAAAGCTGAAAGATGTGTCAACTA 272

RESULT 6

US-10-156-761-2671
; Sequence 2671, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIDA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-25
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2671
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)


```

: APPLICANT: Ogawa, Satoshi
: APPLICANT: Sakurada, Kazuhiko
: APPLICANT: Gojo, Satoshi
: APPLICANT: Yamada, Yoji
: TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDI
: FILE REFERENCE: 00766, 000043
: CURRENT APPLICATION NUMBER: US/09/749, 728B
: CURRENT FILING DATE: 2001-09-17
: PRIOR APPLICATION NUMBER: H11-372826
: PRIOR FILING DATE: 1999-12-28
: PRIOR APPLICATION NUMBER: PCT-JP00-01148
: PRIOR FILING DATE: 2000-02-28
: PRIOR APPLICATION NUMBER: PCT-JP00-07741
: PRIOR FILING DATE: 2000-11-02
: NUMBER OF SEQ ID NOS: 80
: SOFTWARE: PatentIn Ver.2.0
: SEQ ID NO 12
: LENGTH: 1326
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: OTHER INFORMATION: (1)..(1329)
US-09-749-728B-12

Query Match 6.5%; Score 39; DB 10; Length 1326;
Best Local Similarity 56.4%; Pred. No. 0.021;
Matches 92; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

: APPLICANT: Lillie, James
: APPLICANT: Xu, Yongyao
: APPLICANT: Wang, Youzhen
: APPLICANT: Steinmann, Kathleen
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
: TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: TITLE OF INVENTION: THERAPY OF BREAST CANCER
: FILE REFERENCE: MRI-049
: CURRENT APPLICATION NUMBER: US/10/198,846
: CURRENT FILING DATE: 2002-07-18
: PRIOR APPLICATION NUMBER: 60/306,220
: PRIOR FILING DATE: 2001-07-18
: NUMBER OF SEQ ID NOS: 14084
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9872
: LENGTH: 3411
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1, 2, 3
: OTHER INFORMATION: n = A,T,C or G
US-10-198-846-9872

Query Match 6.5%; Score 39; DB 14; Length 3411;
Best Local Similarity 56.4%; Pred. No. 0.021;
Matches 92; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

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Matches 92; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

OY 235 AAGTCCACCTGACCAAGGCTCAGGCGCTGTTAAACCCCTTCCAGATGTGTTTC 294
1100 AAGACCGGCTGTGCAAGAGGCGCGGCGCGGCTGCGCCAGCAAGCGCGCC 1041

OY 295 GTGAGGCTATGAATGCTCCGCGAAGGCTGTGAACCTACCGGCTTCTCCGTGAGCG 354
1040 AGCTCGGCGCATGTAAACCGGCTGTAGGGCTGTGAG-TAGAGACCGCGAAGCGCGCGCC 982

OY 355 GTCAAGCGCGCGCGCTGCGACCGCGCAACCGCGCACTGGCG 397
981 GTACTGCTCGGCGCGCGCGCAAGCGCGCGCGCTCGCGCG 939

DB

RESULT 12
US-09-815-242-7900
Sequence 7900, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlson, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7900
LENGTH: 696
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(696)
US-09-815-242-7900

Query Match
Best Local Similarity 48.6%; Score 38.4; DB 9; Length 696;
Pred. No. 0.024;
Matches 105; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

OY 248 CCAAGCTCAGCGGCGGCTGTAAAGCTCCAGGATGCTGTGAGGCTATGA 307
80 CCAAGCTGTGCGCGGCTGTCAACCAATCAAGGATCCGTGACGTTGCCGTGA 139

DB 308 AGTCCGCGGAGGCGCTGAAGCTCACCGGCTGTCTCCGCTGACGCGTCAAGCGCGG 367
140 ACTCGGCGCTGATCCGCGGCTGAATCCGACGATGCTGTGCGGCGCACGCTCTGCGGA 199

OY 368 CTGCGACCGCGCGCAACCGCGCACTGCGAGCAGATGACATTCGCGGCTTCTCAAGCGG 427
200 ACGCAGCGCGCAAGAGGCTCGCGCTTCCCTTACCAAGGTCGCGGCTCCGAAGCGG 259

DB

OY 428 TTCGATCTCCGCTGCGCTCCCTGCTGTAAGAGCGCG 463
DB 260 CTCTGCTGCTCCGCGCGCGCAAGAGTGGGTATGAGG 295

RESULT 13
US-10-205-979-26
Sequence 26, Application US/10205979
Publication No. US20030147861A1

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
APPLICANT: Abernethy, Nevin
TITLE OF INVENTION: Compounds and Methods for the Modulation
FILE REFERENCE: 11000.10630
CURRENT APPLICATION NUMBER: US/10/205,979
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/308,446
PRIOR FILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 858
TYPE: DNA
ORGANISM: Mycobacterium vaccae
US-10-205-979-26

Query Match
Best Local Similarity 46.3%; Score 37.6; DB 12; Length 858;
Pred. No. 0.051;
Matches 124; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

OY 202 AACAGCTGACCTGTTGCAAGATGCGCCAGAGTCCAACTGACCAAGGCTCAGGCC 261
187 AACAAAGCAGAGCTCATGACGACTACTGACAGAACCTGGGCTCGGATCGTCCGAAAGC 246

DB 262 GAGGCTGCTGTAAAGCTTCCAGAGTGTGCTGAGGCTATGAAGTCCGCGGAAGC 321
247 ACTGCGGCGGTGGAAGAACGTTGTGACACCATGCTGCGCGCCCTGCAAGAGGTGAGAGC 306

OY 322 CTGAAGCTCACCGCGCTGTCTCCGCTGAGCGGCTCAAGCGCCCGCTGACCGCGCG 381
307 GTCACCATCAAGCGGCTTCCGCTGTTCGACAGCAGTGTGCGCAGACGCGTGGACG 366

DB 382 AACCGCGCACCTGCGGAGCAGATGACATTCGCGCTTCTCAAGCGGCTGATCTCCGCT 441
367 AATCCGCGCACCGCGGAGACCGTGAAGGTCAAGCCCACTGATCCCGGATTCGCTCC 426

OY 442 GGCTCCCTGCTGAAGAGGCGGTACCG 469
427 GCGGCTGATTCAGAGCTGTGTCTCTG 454

DB

RESULT 14
US-10-051-643-200
Sequence 200, Application US/10051643
Publication No. US20020197265A1

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
FILE REFERENCE: 11000.10082
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 200
LENGTH: 858
TYPE: DNA
ORGANISM: Mycobacterium vaccae
US-10-051-643-200

Query Match
Best Local Similarity 46.3%; Score 37.6; DB 13; Length 858;
Matches 124; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

OY 202 AACAAAGTGTGACCTGCTTCCAGAGTCCGCCAAGATCCAAAGCTGACAGCC 261
DB 187 AACAAAGTGTGACCTGCTTCCAGAGTCCGCCAAGATCCAAAGCTGACAGCC 246
OY 262 GAGGCTGCTTAAAGCTTCCAGAGTGTTCCTGAGGCTATGATGATCCGCGCAAGCC 321
DB 247 ACTGCGGGGCTGGAGAAAGCTGTGACACCAATCGCGCGCTGCACAAAGGTTGAGAGC 306
OY 322 CTGAAGCTACACGGCTGCTTCCGCTGAGCGCGCTGCAAGCGCGCTGCGACGCGCGC 381
DB 307 GTCAACATCAAGGGCTTGGTGTTCGAGCAGCGCTGCGCGCGCTGCGACGCGCGC 366
OY 382 AACCGCGGCACTGCGGAGAGCAATGACATTCGCGCTTCTACGGCGTTGATCTCCGCT 441
DB 367 AATCCGGCGACCGCGGAGACCGGTCAAGGCCCACTCAGTCCGCGCATTCGCTCC 426
OY 442 GGCCTCCTGCTGAAGAAGCGCGTCACCG 469
DB 427 GCGCTCAAGTTCAAGCGCTGTCTCTG 454

RESULT 15
US-10-156-761-6834

Sequence 6834, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:

APPLICANT: OMDRA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6834
LENGTH: 1089
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1089)
US-10-156-761-6834

Query Match
Best Local Similarity 48.2%; Score 37.6; DB 14; Length 1089;
Matches 106; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

OY 252 GGCCTCAGGCGGAGGCTGCTTAAAGCTTCCAGAGATGTTGCTGAGGCTATGAAGTC 311
DB 516 GGGCTGTGATCTGCTGCTCAACGACTACGTCTCCGGCTGCGCGAGATCAAGAGC 575
OY 312 CGCGAAGCGCTGAAGCTACCGCGGTCTCCGCTGAGCGCGCTCAAGCGCGCGCTCG 371
DB 576 CGGCTTCATGCGCGAGCCGCGGATCTGAGAGTCATGAGCGCGCGCAAGCGCGCG 635

OY 372 CACCGCGCGCAACCGGCACTGGCGAGACATGACATTCGCGCTTCTAAGGCGTTG 431
DB 636 CACTCCCGCGGAGACCGCACACCGCGGAGCTGATCGAGCGCTCCATCAAGAGCGCGA 695
OY 432 TATCTCCGCTGCTCCGCTGGAAGAAGCGCGTACCGAG 471
DB 696 GGTCTCTCCGCGGACCTCAAGAGTGGCGCTGCGCGAG 735

Search completed: August 25, 2003, 22:04:19
Job time : 254.619 secs